



SEQUENCE LISTING

<110> Umezawa, Akihiro

Hata, Jun-Ichi

Fukuda, Keiichi

Ogawa, Satoshi

Sakurada, Kazuhiro

Gojo, Satoshi

Yamada, Yoji

<120> THE CELL HAVING THE POTENTIALITY OF DIFFERENTIATION INTO CARDIOMYOCYTES

<130> 00766.000043

<140> US/09/749,728

<141> 2001-09-17

<150> H11-372826

<151> 1999-12-28

<150> PCT-JP00-01148

<151> 2000-02-28

<150> PCT-JP00-07741

<151> 2000-11-02

<160> 80

<170> PatentIn Ver.2.0

<210> 1

<211> 411

<212> PRT

<213> Homo sapiens

<400> 1

Met Arg Ala His Pro Gly Gly Gly Arg Cys Cys Pro Glu Gln Glu Glu

1 5 10 15

Gly Glu Ser Ala Ala Gly Gly Ser Gly Ala Gly Gly Asp Ser Ala Ile

20 25 30

Glu Gln Gly Gly Gln Gly Ser Ala Leu Ala Pro Ser Pro Val Ser Gly

35 40 45

Val Arg Arg Glu Gly Ala Arg Gly Gly Gly Arg Gly Arg Gly Trp

50 55 60

Lys Gln Ala Gly Arg Gly Gly Gly Val Cys Gly Arg Gly Arg Gly Arg

65 70 75 80

Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg

85 90 95
 Pro Pro Ser Gly Gly Ser Gly Leu Gly Gly Asp Gly Gly Gly Cys Gly
 100 105 110
 Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Arg Arg Glu Pro Val Pro
 115 120 125
 Phe Pro Ser Gly Ser Ala Gly Pro Gly Pro Arg Gly Pro Arg Ala Thr
 130 135 140
 Glu Ser Gly Lys Arg Met Asp Cys Pro Ala Leu Pro Pro Gly Trp Lys
 145 150 155 160
 Lys Glu Glu Val Ile Arg Lys Ser Gly Leu Ser Ala Gly Lys Ser Asp
 165 170 175
 Val Tyr Tyr Phe Ser Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln
 180 185 190
 Leu Ala Arg Tyr Leu Gly Asn Thr Val Asp Leu Ser Ser Phe Asp Phe
 195 200 205
 Arg Thr Gly Lys Met Met Pro Ser Lys Leu Gln Lys Asn Lys Gln Arg
 210 215 220
 Leu Arg Asn Asp Pro Leu Asn Gln Asn Lys Gly Lys Pro Asp Leu Asn
 225 230 235 240
 Thr Thr Leu Pro Ile Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val
 245 250 255
 Thr Lys Val Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln
 260 265 270
 Arg Met Asn Glu Gln Pro Arg Gln Leu Phe Trp Glu Lys Arg Leu Gln
 275 280 285
 Gly Leu Ser Ala Ser Asp Val Thr Glu Gln Ile Ile Lys Thr Met Glu
 290 295 300
 Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Gly Ser Asn Asp Glu Thr
 305 310 315 320
 Leu Leu Ser Ala Val Ala Ser Ala Leu His Thr Ser Ser Ala Pro Ile
 325 330 335
 Thr Gly Gln Val Ser Ala Ala Val Glu Lys Asn Pro Ala Val Trp Leu
 340 345 350
 Asn Thr Ser Gln Pro Leu Cys Lys Ala Phe Ile Val Thr Asp Glu Asp
 355 360 365
 Ile Arg Lys Gln Glu Glu Arg Val Gln Gln Val Arg Lys Lys Leu Glu
 370 375 380
 Glu Ala Leu Met Ala Asp Ile Leu Ser Arg Ala Ala Asp Thr Glu Glu
 385 390 395 400
 Met Asp Ile Glu Met Asp Ser Gly Asp Glu Ala
 405 410

<210> 2

<211> 1233

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1236)

<400> 2

```
atg cgc gcg cac ccg ggg gga ggc cgc tgc tgc ccg gag cag gag gag  48
Met Arg Ala His Pro Gly Gly Gly Arg Cys Cys Pro Glu Gln Glu Glu
   1       5       10      15
ggg gag agt gcg gcg ggc ggc agc ggc gct ggc ggc gac tcc gcc ata  96
Gly Glu Ser Ala Ala Gly Gly Ser Gly Ala Gly Gly Asp Ser Ala Ile
   20      25      30
gag cag ggg ggc cag ggc agc gcg ctc gcc ccg tcc ccg gtg agc ggc  144
Glu Gln Gly Gly Gln Gly Ser Ala Leu Ala Pro Ser Pro Val Ser Gly
   35      40      45
gtg cgc agg gaa ggc gct cgg ggc ggc ggc cgt ggc cgg ggg cgg tgg  192
Val Arg Arg Glu Gly Ala Arg Gly Gly Gly Arg Gly Arg Gly Arg Trp
   50      55      60
aag cag gcg ggc cgg ggc ggc ggc gtc tgt ggc cgt ggc cgg ggc cgg  240
Lys Gln Ala Gly Arg Gly Gly Gly Val Cys Gly Arg Gly Arg Gly Arg
   65      70      75      80
ggc cgt ggc cgg gga cgg gga cgg ggc cgg ggc cgg ggc cgc ggc cgt  288
Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg
   85      90      95
ccc ccg agt ggc ggc agc ggc ctt ggc ggc gac ggc ggc ggc tgc ggc  336
Pro Pro Ser Gly Gly Ser Gly Leu Gly Gly Asp Gly Gly Gly Cys Gly
  100     105     110
ggc ggc ggc agc ggt ggc ggc ggc gcc ccc cgg cgg gag ccg gtc cct  384
Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Arg Arg Glu Pro Val Pro
  115     120     125
ttc ccg tcg ggg agc gcg ggg ccg ggg ccc agg gga ccc cgg gcc acg  432
Phe Pro Ser Gly Ser Ala Gly Pro Gly Pro Arg Gly Pro Arg Ala Thr
  130     135     140
gag agc ggg aag agg atg gat tgc ccg gcc ctc ccc ccc gga tgg aag  480
Glu Ser Gly Lys Arg Met Asp Cys Pro Ala Leu Pro Pro Gly Trp Lys
  145     150     155     160
aag gag gaa gtg atc cga aaa tct ggg cta agt gct ggc aag agc gat  528
Lys Glu Glu Val Ile Arg Lys Ser Gly Leu Ser Ala Gly Lys Ser Asp
  165     170     175
gtc tac tac ttc agt cca agt ggt aag aag ttc aga agc aag cct cag  576
Val Tyr Tyr Phe Ser Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln
  180     185     190
ttg gca agg tac ctg gga aat act gtt gat ctc agc agt ttt gac ttc  624
Leu Ala Arg Tyr Leu Gly Asn Thr Val Asp Leu Ser Ser Phe Asp Phe
  195     200     205
aga act gga aag atg atg cct agt aaa tta cag aag aac aaa cag aga  672
Arg Thr Gly Lys Met Met Pro Ser Lys Leu Gln Lys Asn Lys Gln Arg
  210     215     220
ctg cga aac gat cct ctc aat caa aat aag ggt aaa cca gac ttg aat  720
```

Leu Arg Asn Asp Pro Leu Asn Gln Asn Lys Gly Lys Pro Asp Leu Asn
225 230 235 240

aca aca ttg cca att aga caa aca gca tca att ttc aaa caa ccg gta 768

Thr Thr Leu Pro Ile Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val
245 250 255

acc aaa gtc aca aat cat cct agt aat aaa gtg aaa tca gac cca caa 816

Thr Lys Val Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln
260 265 270

cga atg aat gaa cag cca cgt cag ctt ttc tgg gag aag agg cta caa 864

Arg Met Asn Glu Gln Pro Arg Gln Leu Phe Trp Glu Lys Arg Leu Gln
275 280 285

gga ctt agt gca tca gat gta aca gaa caa att ata aaa acc atg gaa 912

Gly Leu Ser Ala Ser Asp Val Thr Glu Gln Ile Ile Lys Thr Met Glu
290 295 300

cta ccc aaa ggt ctt caa gga gtt ggt cca ggt agc aat gat gag acc 960

Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Gly Ser Asn Asp Glu Thr
305 310 315 320

ctt tta tct get gtt gcc agt gct ttg cac aca agc tct gcg cca atc 1008

Leu Leu Ser Ala Val Ala Ser Ala Leu His Thr Ser Ser Ala Pro Ile
325 330 335

aca ggg caa gtc tcc get get gtg gaa aag aac cct gct gtt tgg ctt 1056

Thr Gly Gln Val Ser Ala Ala Val Glu Lys Asn Pro Ala Val Trp Leu
340 345 350

aac aca tct caa ccc ctc tgc aaa get ttt att gtc aca gat gaa gac 1104

Asn Thr Ser Gln Pro Leu Cys Lys Ala Phe Ile Val Thr Asp Glu Asp
355 360 365

atc agg aaa cag gaa gag cga gta cag caa gta cgc aag aaa ttg gaa 1152

Ile Arg Lys Gln Glu Glu Arg Val Gln Gln Val Arg Lys Lys Leu Glu
370 375 380

gaa gca ctg atg gca gac atc ttg teg cga get get gat aca gaa gag 1200

Glu Ala Leu Met Ala Asp Ile Leu Ser Arg Ala Ala Asp Thr Glu Glu
385 390 395 400

atg gat att gaa atg gac agt gga gat gaa gcc 1233

Met Asp Ile Glu Met Asp Ser Gly Asp Glu Ala
405 410

<210> 3

<211> 196

<212> PRT

<213> Homo sapiens

<400> 3

Met Arg Thr Leu Ala Cys Leu Leu Leu Leu Gly Cys Gly Tyr Leu Ala

1 5 10 15

His Val Leu Ala Glu Glu Ala Glu Ile Pro Arg Glu Val Ile Glu Arg

20 25 30

Leu Ala Arg Ser Gln Ile His Ser Ile Arg Asp Leu Gln Arg Leu Leu

35 40 45

Glu Ile Asp Ser Val Gly Ser Glu Asp Ser Leu Asp Thr Ser Leu Arg
 50 55 60
 Ala His Gly Val His Ala Thr Lys His Val Pro Glu Lys Arg Pro Leu
 65 70 75 80
 Pro Ile Arg Arg Lys Arg Ser Ile Glu Glu Ala Val Pro Ala Val Cys
 85 90 95
 Lys Thr Arg Thr Val Ile Tyr Glu Ile Pro Arg Ser Gln Val Asp Pro
 100 105 110
 Thr Ser Ala Asn Phe Leu Ile Trp Pro Pro Cys Val Glu Val Lys Arg
 115 120 125
 Cys Thr Gly Cys Cys Asn Thr Ser Ser Val Lys Cys Gln Pro Ser Arg
 130 135 140
 Val His His Arg Ser Val Lys Val Ala Lys Val Glu Tyr Val Arg Lys
 145 150 155 160
 Lys Pro Lys Leu Lys Glu Val Gln Val Arg Leu Glu Glu His Leu Glu
 165 170 175
 Cys Ala Cys Ala Thr Thr Ser Leu Asn Pro Asp Tyr Arg Glu Glu Asp
 180 185 190
 Thr Asp Val Arg
 195

<210> 4

<211> 588

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(591)

<400> 4

atg agg acc ttg gct tgc ctg ctg ctc ctc ggc tgc gga tac ctc gcc 48
 Met Arg Thr Leu Ala Cys Leu Leu Leu Leu Gly Cys Gly Tyr Leu Ala
 1 5 10 15
 cat gtt ctg gcc gag gaa gcc gag atc ccc cgc gag gtg atc gag agg 96
 His Val Leu Ala Glu Glu Ala Glu Ile Pro Arg Glu Val Ile Glu Arg
 20 25 30
 ctg gcc cgc agt cag atc cac agc atc cgg gac ctc cag cga ctc ctg 144
 Leu Ala Arg Ser Gln Ile His Ser Ile Arg Asp Leu Gln Arg Leu Leu
 35 40 45
 gag ata gac tcc gta ggg agt gag gat tct ttg gac acc agc ctg aga 192
 Glu Ile Asp Ser Val Gly Ser Glu Asp Ser Leu Asp Thr Ser Leu Arg
 50 55 60
 gct cac ggg gtc cac gcc act aag cat gtg ccc gag aag cgg ccc ctg 240
 Ala His Gly Val His Ala Thr Lys His Val Pro Glu Lys Arg Pro Leu
 65 70 75 80
 ccc att cgg agg aag aga agc atc gag gaa gct gtc ccc gct gtc tgc 288
 Pro Ile Arg Arg Lys Arg Ser Ile Glu Glu Ala Val Pro Ala Val Cys
 85 90 95

aag acc agg acg gtc att tac gag att cct cgg agt cag gtc gac ccc 336
Lys Thr Arg Thr Val Ile Tyr Glu Ile Pro Arg Ser Gln Val Asp Pro

100 105 110

acg tcc gcc aac ttc ctg atc tgg ccc ccg tgc gtg gag gtg aaa cgc 384
Thr Ser Ala Asn Phe Leu Ile Trp Pro Pro Cys Val Glu Val Lys Arg

115 120 125

tgc acc ggc tgc tgc aac acg agc agt gtc aag tgc cag ccc tcc cgc 432
Cys Thr Gly Cys Cys Asn Thr Ser Ser Val Lys Cys Gln Pro Ser Arg

130 135 140

gtc cac cac cgc agc gtc aag gtg gcc aag gtg gaa tac gtc agg aag 480
Val His His Arg Ser Val Lys Val Ala Lys Val Glu Tyr Val Arg Lys

145 150 155 160

aag cca aaa tta aaa gaa gtc cag gtg agg tta gag gag cat ttg gag 528
Lys Pro Lys Leu Lys Glu Val Gln Val Arg Leu Glu Glu His Leu Glu

165 170 175

tgc gcc tgc gcg acc aca agc ctg aat ccg gat tat cgg gaa gag gac 576
Cys Ala Cys Ala Thr Thr Ser Leu Asn Pro Asp Tyr Arg Glu Glu Asp

180 185 190

• acg gat gtg agg 588

Thr Asp Val Arg

195

<210> 5

<211> 241

<212> PRT

<213> Homo sapiens

<400> 5

• Met Asn Arg Cys Trp Ala Leu Phe Leu Ser Leu Cys Cys Tyr Leu Arg

1 5 10 15

• Leu Val Ser Ala Glu Gly Asp Pro Ile Pro Glu Glu Leu Tyr Glu Met

20 25 30

Leu Ser Asp His Ser Ile Arg Ser Phe Asp Asp Leu Gln Arg Leu Leu

35 40 45

His Gly Asp Pro Gly Glu Glu Asp Gly Ala Glu Leu Asp Leu Asn Met

50 55 60

Thr Arg Ser His Ser Gly Gly Glu Leu Glu Ser Leu Ala Arg Gly Arg

65 70 75 80

Arg Ser Leu Gly Ser Leu Thr Ile Ala Glu Pro Ala Met Ile Ala Glu

85 90 95

Cys Lys Thr Arg Thr Glu Val Phe Glu Ile Ser Arg Arg Leu Ile Asp

100 105 110

Arg Thr Asn Ala Asn Phe Leu Val Trp Pro Pro Cys Val Glu Val Gln

115 120 125

Arg Cys Ser Gly Cys Cys Asn Asn Arg Asn Val Gln Cys Arg Pro Thr

130 135 140

Gln Val Gln Leu Arg Pro Val Gln Val Arg Lys Ile Glu Ile Val Arg

145 150 155 160

Lys Lys Pro Ile Phe Lys Lys Ala Thr Val Thr Leu Glu Asp His Leu
 165 170 175
 Ala Cys Lys Cys Glu Thr Val Ala Ala Arg Pro Val Thr Arg Ser
 180 185 190
 Pro Gly Gly Ser Gln Glu Gln Arg Ala Lys Thr Pro Gln Thr Arg Val
 195 200 205
 Thr Ile Arg Thr Val Arg Val Arg Arg Pro Pro Lys Gly Lys His Arg
 210 215 220
 Lys Phe Lys His Thr His Asp Lys Thr Ala Leu Lys Glu Thr Leu Gly
 225 230 235 240

Ala

<210> 6

<211> 723

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(726)

<400> 6

atg aat cgc tgc tgg gcg ctc ttc ctg tct ctc tgc tgc tac ctg cgt 48
 Met Asn Arg Cys Trp Ala Leu Phe Leu Ser Leu Cys Cys Tyr Leu Arg
 1 5 10 15
 ctg gtc agc gcc gag ggg gac ccc att ccc gag gag ctt tat gag atg 96
 Leu Val Ser Ala Glu Gly Asp Pro Ile Pro Glu Glu Leu Tyr Glu Met
 20 25 30
 ctg agt gac cac tcg atc cgc tcc ttt gat gat ctc caa cgc ctg ctg 144
 Leu Ser Asp His Ser Ile Arg Ser Phe Asp Asp Leu Gln Arg Leu Leu
 35 40 45
 cac gga gac ccc gga gag gaa gat ggg gcc gag ttg gac ctg aac atg 192
 His Gly Asp Pro Gly Glu Glu Asp Gly Ala Glu Leu Asp Leu Asn Met
 50 55 60
 acc cgc tcc cac tct gga ggc gag ctg gag agc ttg gct cgt gga aga 240
 Thr Arg Ser His Ser Gly Gly Glu Leu Glu Ser Leu Ala Arg Gly Arg
 65 70 75 80
 agg agc ctg ggt tcc ctg acc att gct gag ccg gcc atg atc gcc gag 288
 Arg Ser Leu Gly Ser Leu Thr Ile Ala Glu Pro Ala Met Ile Ala Glu
 85 90 95
 tgc aag acg cgc acc gag gtg ttc gag atc tcc cgg cgc ctc ata gac 336
 Cys Lys Thr Arg Thr Glu Val Phe Glu Ile Ser Arg Arg Leu Ile Asp
 100 105 110
 cgc acc aac gcc aac ttc ctg gtg tgg ccg ccc tgt gtg gag gtg cag 384
 Arg Thr Asn Ala Asn Phe Leu Val Trp Pro Pro Cys Val Glu Val Gln
 115 120 125
 cgc tgc tcc ggc tgc tgc aac aac cgc aac gtg cag tgc cgc ccc acc 432
 Arg Cys Ser Gly Cys Cys Asn Asn Arg Asn Val Gln Cys Arg Pro Thr
 130 135 140

cag gtg cag ctg cga cct gtc cag gtg aga aag atc gag att gtg cgg 480
 Gln Val Gln Leu Arg Pro Val Gln Val Arg Lys Ile Glu Ile Val Arg
 145 150 155 160
 aag aag cca atc ttt aag aag gcc acg gtg acg ctg gaa gac cac ctg 528
 Lys Lys Pro Ile Phe Lys Lys Ala Thr Val Thr Leu Glu Asp His Leu
 165 170 175
 gca tgc aag tgt gag aca gtg gca gct gca cgg cct gtg acc cga agc 576
 Ala Cys Lys Cys Glu Thr Val Ala Ala Ala Arg Pro Val Thr Arg Ser
 180 185 190
 ccg ggg ggt tcc cag gag cag cga gcc aaa acg ccc caa act cgg gtg 624
 Pro Gly Gly Ser Gln Glu Gln Arg Ala Lys Thr Pro Gln Thr Arg Val
 195 200 205
 acc att cgg acg gtg cga gtc cgc cgg ccc ccc aag ggc aag cac cgg 672
 Thr Ile Arg Thr Val Arg Val Arg Arg Pro Pro Lys Gly Lys His Arg
 210 215 220
 aaa ttc aag cac acg cat gac aag acg gca ctg aag gag acc ctt gga 720
 Lys Phe Lys His Thr His Asp Lys Thr Ala Leu Lys Glu Thr Leu Gly
 225 230 235 240
 gcc 723
 Ala
 <210> 7
 <211> 155
 <212> PRT
 <213> Homo sapiens
 <400> 7
 Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp Gly
 1 5 10 15
 Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu
 20 25 30
 Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg
 35 40 45
 Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu
 50 55 60
 Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn
 65 70 75 80
 Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys
 85 90 95
 Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr
 100 105 110
 Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys
 115 120 125
 Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys
 130 135 140
 Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser
 145 150 155
 <210> 8

<211> 465

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(468)

<400> 8

atg gca gcc ggg agc atc acc acg ctg ccc gcc ttg ccc gag gat ggc 48

Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp Gly

1 5 10 15

ggc agc ggc gcc ttc ccg ccc ggc cac ttc aag gac ccc aag cgg ctg 96

Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu

20 25 30

tac tgc aaa aac ggg ggc ttc ttc ctg cgc atc cac ccc gac ggc cga 144

Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg

35 40 45

gtt gac ggg gtc cgg gag aag agc gac cct cac atc aag cta caa ctt 192

Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu

50 55 60

caa gca gaa gag aga gga gtt gtg tct atc aaa gga gtg tgt gct aac 240

Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn

65 70 75 80

cgt tac ctg gct atg aag gaa gat gga aga tta ctg gct tct aaa tgt 288

Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys

85 90 95

gtt acg gat gag tgt ttc ttt ttt gaa cga ttg gaa tct aat aac tac 336

Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr

100 105 110

aat act tac cgg tca agg aaa tac acc agt tgg tat gtg gca ttg aaa 384

Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys

115 120 125

cga act ggg cag tat aaa ctt gga tcc aaa aca gga cct ggg cag aaa 432

Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys

130 135 140

gct ata ctt ttt ctt cca atg tct gct aag agc 465

Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser

145 150 155

<210> 9

<211> 324

<212> PRT

<213> Homo sapiens

<400> 9

Met Phe Pro Ser Pro Ala Leu Thr Pro Thr Pro Phe Ser Val Lys Asp

1 5 10 15

Ile Leu Asn Leu Glu Gln Gln Gln Arg Ser Leu Ala Ala Ala Gly Glu

20 25 30

Leu Ser Ala Arg Leu Glu Ala Thr Leu Ala Pro Ser Ser Cys Met Leu
 35 40 45
 Ala Ala Phe Lys Pro Glu Ala Tyr Ala Gly Pro Glu Ala Ala Ala Pro
 50 55 60
 Gly Leu Pro Glu Leu Arg Ala Glu Leu Gly Arg Ala Pro Ser Pro Ala
 65 70 75 80
 Lys Cys Ala Ser Ala Phe Pro Ala Ala Pro Ala Phe Tyr Pro Arg Ala
 85 90 95
 Tyr Ser Asp Pro Asp Pro Ala Lys Asp Pro Arg Ala Glu Lys Lys Glu
 100 105 110
 Leu Cys Ala Leu Gln Lys Ala Val Glu Leu Glu Lys Thr Glu Ala Asp
 115 120 125
 Asn Ala Glu Arg Pro Arg Ala Arg Arg Arg Lys Pro Arg Val Leu
 130 135 140
 Phe Ser Gln Ala Gln Val Tyr Glu Leu Glu Arg Arg Phe Lys Gln Gln
 145 150 155 160
 Arg Tyr Leu Ser Ala Pro Glu Arg Asp Gln Leu Ala Ser Val Leu Lys
 165 170 175
 Leu Thr Ser Thr Gln Val Lys Ile Trp Phe Gln Asn Arg Arg Tyr Lys
 180 185 190
 Cys Lys Arg Gln Arg Gln Asp Gln Thr Leu Glu Leu Val Gly Leu Pro
 195 200 205
 Pro Pro Pro Pro Pro Pro Ala Arg Arg Ile Ala Val Pro Val Leu Val
 210 215 220
 Arg Asp Gly Lys Pro Cys Leu Gly Asp Ser Ala Pro Tyr Ala Pro Ala
 225 230 235 240
 Tyr Gly Val Gly Leu Asn Pro Tyr Gly Tyr Asn Ala Tyr Pro Ala Tyr
 245 250 255
 Pro Gly Tyr Gly Gly Ala Ala Cys Ser Pro Gly Tyr Ser Cys Thr Ala
 260 265 270
 Ala Tyr Pro Ala Gly Pro Ser Pro Ala Gln Pro Ala Thr Ala Ala Ala
 275 280 285
 Asn Asn Asn Phe Val Asn Phe Gly Val Gly Asp Leu Asn Ala Val Gln
 290 295 300
 Ser Pro Gly Ile Pro Gln Ser Asn Ser Gly Val Ser Thr Leu His Gly
 305 310 315 320
 Ile Arg Ala Trp

<210> 10

<211> 972

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(975)

<400> 10

atg ttc ccc agc cct gct ctc acg ccc acg ccc ttc tca gtc aaa gac 48
 Met Phe Pro Ser Pro Ala Leu Thr Pro Thr Pro Phe Ser Val Lys Asp
 1 5 10 15
 atc cta aac ctg gaa cag cag cag cgc agc ctg gct gcc gcc gga gag 96
 Ile Leu Asn Leu Glu Gln Gln Gln Arg Ser Leu Ala Ala Ala Gly Glu
 20 25 30
 ctc tct gcc cgc ctg gag gcg acc ctg gcg ccc tcc tcc tgc atg ctg 144
 Leu Ser Ala Arg Leu Glu Ala Thr Leu Ala Pro Ser Ser Cys Met Leu
 35 40 45
 gcc gcc ttc aag cca gag gcc tac gct ggg ccc gag gcg gct gcg ccg 192
 Ala Ala Phe Lys Pro Glu Ala Tyr Ala Gly Pro Glu Ala Ala Ala Pro
 50 55 60
 ggc ctc cca gag ctg cgc gca gag ctg ggc cgc gcg cct tca ccg gcc 240
 Gly Leu Pro Glu Leu Arg Ala Glu Leu Gly Arg Ala Pro Ser Pro Ala
 65 70 75 80
 aag tgt gcg tct gcc ttt ccc gcc gcc ccc gcc ttc tat cca cgt gcc 288
 Lys Cys Ala Ser Ala Phe Pro Ala Ala Pro Ala Phe Tyr Pro Arg Ala
 85 90 95
 tac agc gac ccc gac cca gcc aag gac cct aga gcc gaa aag aaa gag 336
 Tyr Ser Asp Pro Asp Pro Ala Lys Asp Pro Arg Ala Glu Lys Lys Glu
 100 105 110
 ctg tgc gcg ctg cag aag gcg gtg gag ctg gag aag aca gag gcg gac 384
 Leu Cys Ala Leu Gln Lys Ala Val Glu Leu Glu Lys Thr Glu Ala Asp
 115 120 125
 aac gcg gag cgg ccc cgg gcg cga cgg cgg agg aag ccg cgc gtg ctc 432
 Asn Ala Glu Arg Pro Arg Ala Arg Arg Arg Arg Lys Pro Arg Val Leu
 130 135 140
 ttc tcg cag gcg cag gtc tat gag ctg gag cgg cgc ttc aag cag cag 480
 Phe Ser Gln Ala Gln Val Tyr Glu Leu Glu Arg Arg Phe Lys Gln Gln
 145 150 155 160
 cgg tac ctg tcg gcc ccc gaa cgc gac cag ctg gcc agc gtg ctg aaa 528
 Arg Tyr Leu Ser Ala Pro Glu Arg Asp Gln Leu Ala Ser Val Leu Lys
 165 170 175
 ctc acg tcc acg cag gtc aag atc tgg ttc cag aac cgg cgc tac aag 576
 Leu Thr Ser Thr Gln Val Lys Ile Trp Phe Gln Asn Arg Arg Tyr Lys
 180 185 190
 tgc aag cgg cag cgg cag gac cag act ctg gag ctg gtg ggg ctg ccc 624
 Cys Lys Arg Gln Arg Gln Asp Gln Thr Leu Glu Leu Val Gly Leu Pro
 195 200 205
 ccg ccg ccg ccg ccg cct gcc cgc agg atc gcg gtg cca gtg ctg gtg 672
 Pro Pro Pro Pro Pro Ala Arg Arg Ile Ala Val Pro Val Leu Val
 210 215 220
 cgc gat ggc aag cca tgc cta ggg gac tcg gcg ccc tac gcg cct gcc 720
 Arg Asp Gly Lys Pro Cys Leu Gly Asp Ser Ala Pro Tyr Ala Pro Ala
 225 230 235 240
 tac ggc gtg ggc ctc aat ccc tac ggt tat aac gcc tac ccc gcc tat 768

Tyr Gly Val Gly Leu Asn Pro Tyr Gly Tyr Asn Ala Tyr Pro Ala Tyr
 245 250 255
 ccg ggt tac ggc ggc gcg gcc tgc agc cct ggc tac agc tgc act gcc 816
 Pro Gly Tyr Gly Gly Ala Ala Cys Ser Pro Gly Tyr Ser Cys Thr Ala
 260 265 270
 gct tac ccc gcc ggg cct tcc cca gcg cag ccg gcc act gcc gcc gcc 864
 Ala Tyr Pro Ala Gly Pro Ser Pro Ala Gln Pro Ala Thr Ala Ala Ala
 275 280 285
 aac aac aac ttc gtg aac ttc ggc gtc ggg gac ttg aat gcg gtt cag 912
 Asn Asn Asn Phe Val Asn Phe Gly Val Gly Asp Leu Asn Ala Val Gln
 290 295 300
 agc ccc ggg att ccg cag agc aac tcg gga gtg tcc acg ctg cat ggt 960
 Ser Pro Gly Ile Pro Gln Ser Asn Ser Gly Val Ser Thr Leu His Gly
 305 310 315 320
 atc cga gcc tgg 972
 Ile Arg Ala Trp
 324
 <210> 11
 <211> 442
 <212> PRT
 <213> Homo sapiens
 <400> 11
 Met Tyr Gln Ser Leu Ala Met Ala Ala Asn His Gly Pro Pro Pro Gly
 1 5 10 15
 Ala Tyr Gln Ala Gly Gly Pro Gly Pro Phe Met His Gly Ala Gly Ala
 20 25 30
 Ala Ser Ser Pro Val Tyr Leu Pro Thr Pro Arg Val Pro Ser Ser Val
 35 40 45
 Leu Gly Leu Ser Tyr Leu Gln Gly Gly Gly Ala Gly Ser Ala Ser Gly
 50 55 60
 Gly Pro Ser Gly Gly Ser Pro Gly Gly Ala Ala Ser Gly Ala Gly Pro
 65 70 75 80
 Gly Thr Gln Gln Gly Ser Pro Gly Trp Ser Gln Ala Gly Ala Thr Gly
 85 90 95
 Ala Ala Tyr Thr Pro Pro Pro Val Ser Pro Arg Phe Ser Phe Pro Gly
 100 105 110
 Thr Thr Gly Ser Leu Ala Ala Ala Ala Ala Ala Ala Arg Glu
 115 120 125
 Ala Ala Ala Tyr Ser Ser Gly Gly Gly Ala Ala Gly Ala Gly Leu Ala
 130 135 140
 Gly Arg Glu Gln Tyr Gly Arg Ala Gly Phe Ala Gly Ser Tyr Ser Ser
 145 150 155 160
 Pro Tyr Pro Ala Tyr Met Ala Asp Val Gly Ala Ser Trp Ala Ala Ala
 165 170 175
 Ala Ala Ala Ser Ala Gly Pro Phe Asp Ser Pro Val Leu His Ser Leu
 180 185 190

Pro Gly Arg Ala Asn Pro Ala Ala Arg His Pro Asn Leu Asp Met Phe
 195 200 205
 Asp Asp Phe Ser Glu Gly Arg Glu Cys Val Asn Cys Gly Ala Met Ser
 210 215 220
 Thr Pro Leu Trp Arg Arg Asp Gly Thr Gly His Tyr Leu Cys Asn Ala
 225 230 235 240
 Cys Gly Leu Tyr His Lys Met Asn Gly Ile Asn Arg Pro Leu Ile Lys
 245 250 255
 Pro Gln Arg Arg Leu Ser Ala Ser Arg Arg Val Gly Leu Ser Cys Ala
 260 265 270
 Asn Cys Gln Thr Thr Thr Thr Thr Leu Trp Arg Arg Asn Ala Glu Gly
 275 280 285
 Glu Pro Val Cys Asn Ala Cys Gly Leu Tyr Met Lys Leu His Gly Val
 290 295 300
 Pro Arg Pro Leu Ala Met Arg Lys Glu Gly Ile Gln Thr Arg Lys Arg
 305 310 315 320
 Lys Pro Lys Asn Leu Asn Lys Ser Lys Thr Pro Ala Ala Pro Ser Gly
 325 330 335
 Ser Glu Ser Leu Pro Pro Ala Ser Gly Ala Ser Ser Asn Ser Ser Asn
 340 345 350
 Ala Thr Thr Ser Ser Ser Glu Glu Met Arg Pro Ile Lys Thr Glu Pro
 355 360 365
 Gly Leu Ser Ser His Tyr Gly His Ser Ser Ser Val Ser Gln Thr Phe
 370 375 380
 Ser Val Ser Ala Met Ser Gly His Gly Pro Ser Ile His Pro Val Leu
 385 390 395 400
 Ser Ala Leu Lys Leu Ser Pro Gln Gly Tyr Ala Ser Pro Val Ser Gln
 405 410 415
 Ser Pro Gln Thr Ser Ser Lys Gln Asp Ser Trp Asn Ser Leu Val Leu
 420 425 430
 Ala Asp Ser His Gly Asp Ile Ile Thr Ala
 435 440

<210> 12

<211> 1326

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1329)

<400> 12

atg tat cag agc ttg gcc atg gcc gcc aac cac ggg ccg ccc ccc ggt 48
 Met Tyr Gln Ser Leu Ala Met Ala Ala Asn His Gly Pro Pro Pro Gly
 1 5 10 15
 gcc tac cag gcg ggc gcc ccc gcc ccc ttc atg cac ggc gcg ggc gcc 96
 Ala Tyr Gln Ala Gly Gly Pro Gly Pro Phe Met His Gly Ala Gly Ala
 20 25 30

gcg tcc tcg cca gtc tac ctg ccc aca ccg cgg gtg ccc tcc tcc gtt 144
 Ala Ser Ser Pro Val Tyr Leu Pro Thr Pro Arg Val Pro Ser Ser Val
 35 40 45
 ctg ggc ctg tcc tac ctc cag ggc gga ggc gcg ggc tct gcg tcc gga 192
 Leu Gly Leu Ser Tyr Leu Gln Gly Gly Gly Ala Gly Ser Ala Ser Gly
 50 55 60
 ggc ccc tcg ggc ggc agc ccc ggt ggg gcc gcg tct ggt gcg ggg ccc 240
 Gly Pro Ser Gly Gly Ser Pro Gly Gly Ala Ala Ser Gly Ala Gly Pro
 65 70 75 80
 ggg acc cag cag ggc agc ccg gga tgg agc cag gcg gga gcg acc gga 288
 Gly Thr Gln Gln Gly Ser Pro Gly Trp Ser Gln Ala Gly Ala Thr Gly
 85 90 95
 gcc gct tac acc ccg ccg ccg gtg tcg ccg cgc ttc tcc ttc ccg ggg 336
 Ala Ala Tyr Thr Pro Pro Pro Val Ser Pro Arg Phe Ser Phe Pro Gly
 100 105 110
 acc acc ggg tcc ctg gcg gcg gcg gcg gcg gct gcc gcc gcc cgg gaa 384
 Thr Thr Gly Ser Leu Ala Ala Ala Ala Ala Ala Ala Ala Arg Glu
 115 120 125
 gct gcg gcc tac agc agt ggc ggc gga gcg gcg ggt gcg ggc ctg gcg 432
 Ala Ala Ala Tyr Ser Ser Gly Gly Gly Ala Ala Gly Ala Gly Leu Ala
 130 135 140
 ggc cgc gag cag tac ggg cgc gcc ggc ttc gcg ggc tcc tac tcc agc 480
 Gly Arg Glu Gln Tyr Gly Arg Ala Gly Phe Ala Gly Ser Tyr Ser Ser
 145 150 155 160
 ccc tac ccg gct tac atg gcc gac gtg ggc gcg tcc tgg gcc gca gcc 528
 Pro Tyr Pro Ala Tyr Met Ala Asp Val Gly Ala Ser Trp Ala Ala Ala
 165 170 175
 gcc gcc gcc tcc gcc ggc ccc ttc gac agc ccg gtc ctg cac agc ctg 576
 Ala Ala Ala Ser Ala Gly Pro Phe Asp Ser Pro Val Leu His Ser Leu
 180 185 190
 ccc ggc cgg gcc aac ccg gcc gcc cga cac ccc aat ctc gat atg ttt 624
 Pro Gly Arg Ala Asn Pro Ala Ala Arg His Pro Asn Leu Asp Met Phe
 195 200 205
 gac gac ttc tca gaa ggc aga gag tgt gtc aac tgt ggg gct atg tcc 672
 Asp Asp Phe Ser Glu Gly Arg Glu Cys Val Asn Cys Gly Ala Met Ser
 210 215 220
 acc ccg ctc tgg agg cga gat ggg acg ggt cac tat ctg tgc aac gcc 720
 Thr Pro Leu Trp Arg Arg Asp Gly Thr Gly His Tyr Leu Cys Asn Ala
 225 230 235 240
 tgt ggc ctc tac cac aag atg aac ggc atc aac cgg ccg ctc atc aag 768
 Cys Gly Leu Tyr His Lys Met Asn Gly Ile Asn Arg Pro Leu Ile Lys
 245 250 255
 cct cag cgc cgg ctg tcc gcc tcc cgc cga gtg ggc ctc tcc tgt gcc 816
 Pro Gln Arg Arg Leu Ser Ala Ser Arg Arg Val Gly Leu Ser Cys Ala
 260 265 270
 aac tgc cag acc acc acc acc acg ctg tgg cgc cgc aat gcg gag ggc 864

Asn Cys Gln Thr Thr Thr Thr Thr Leu Trp Arg Arg Asn Ala Glu Gly
 275 280 285
 gag cct gtg tgc aat gcc tgc ggc ctc tac atg aag ctc cac ggg gtg 912
 Glu Pro Val Cys Asn Ala Cys Gly Leu Tyr Met Lys Leu His Gly Val
 290 295 300
 ccc agg cct ctt gca atg cgg aaa gag ggg atc caa acc aga aaa cgg 960
 Pro Arg Pro Leu Ala Met Arg Lys Glu Gly Ile Gln Thr Arg Lys Arg
 305 310 315 320
 aag ccc aag aac ctg aat aaa tct aag aca cca gca gct cct tca ggc 1008
 Lys Pro Lys Asn Leu Asn Lys Ser Lys Thr Pro Ala Ala Pro Ser Gly
 325 330 335
 agt gag agc ctt cct ccc gcc agc ggt gct tcc agc aac tcc agc aac 1056
 Ser Glu Ser Leu Pro Pro Ala Ser Gly Ala Ser Ser Asn Ser Ser Asn
 340 345 350
 gcc acc acc agc agc agc gag gag atg cgt ccc atc aag acg gag cct 1104
 Ala Thr Thr Ser Ser Ser Glu Glu Met Arg Pro Ile Lys Thr Glu Pro
 355 360 365
 ggc ctg tca tct cac tac ggg cac agc agc tcc gtg tcc cag acg ttc 1152
 Gly Leu Ser Ser His Tyr Gly His Ser Ser Ser Val Ser Gln Thr Phe
 370 375 380
 tca gtc agt gcg atg tct ggc cat ggg ccc tcc atc cac cct gtc ctc 1200
 Ser Val Ser Ala Met Ser Gly His Gly Pro Ser Ile His Pro Val Leu
 385 390 395 400
 tgg gcc ctg aag ctc tcc cca caa ggc tat gcg tct ccc gtc agc cag 1248
 Ser Ala Leu Lys Leu Ser Pro Gln Gly Tyr Ala Ser Pro Val Ser Gln
 405 410 415
 tct cca cag acc agc tcc aag cag gac tct tgg aac agt ctg gtc ttg 1296
 Ser Pro Gln Thr Ser Ser Lys Gln Asp Ser Trp Asn Ser Leu Val Leu
 420 425 430
 gcc gac agt cac ggg gac ata atc act gcg 1326
 Ala Asp Ser His Gly Asp Ile Ile Thr Ala
 435 440
 <210> 13
 <211> 507
 <212> PRT
 <213> Homo sapiens
 <400> 13
 Met Gly Arg Lys Lys Ile Gln Ile Thr Arg Ile Met Asp Glu Arg Asn
 1 5 10 15
 Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala
 20 25 30
 Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe
 35 40 45
 Asn Ser Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys
 50 55 60
 Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr

65 70 75 80
 Asn Ser Asp Ile Val Glu Ala Leu Asn Lys Lys Glu His Arg Gly Cys
 85 90 95
 Asp Ser Pro Asp Pro Asp Thr Ser Tyr Val Leu Thr Pro His Thr Glu
 100 105 110
 Glu Lys Tyr Lys Lys Ile Asn Glu Glu Phe Asp Asn Met Met Arg Asn
 115 120 125
 His Lys Ile Ala Pro Gly Leu Pro Pro Gln Asn Phe Ser Met Ser Val
 130 135 140
 Thr Val Pro Val Thr Ser Pro Asn Ala Leu Ser Tyr Thr Asn Pro Gly
 145 150 155 160
 Ser Ser Leu Val Ser Pro Ser Leu Ala Ala Ser Ser Thr Leu Thr Asp
 165 170 175
 Ser Ser Met Leu Ser Pro Pro Gln Thr Thr Leu His Arg Asn Val Ser
 180 185 190
 Pro Gly Ala Pro Gln Arg Pro Pro Ser Thr Gly Asn Ala Gly Gly Met
 195 200 205
 Leu Ser Thr Thr Asp Leu Thr Val Pro Asn Gly Ala Gly Ser Ser Pro
 210 215 220
 Val Gly Asn Gly Phe Val Asn Ser Arg Ala Ser Pro Asn Leu Ile Gly
 225 230 235 240
 Ala Thr Gly Ala Asn Ser Leu Gly Lys Val Met Pro Thr Lys Ser Pro
 245 250 255
 Pro Pro Pro Gly Gly Gly Asn Leu Gly Met Asn Ser Arg Lys Pro Asp
 260 265 270
 Leu Arg Val Val Ile Pro Pro Ser Ser Lys Gly Met Met Pro Pro Leu
 275 280 285
 Ser Glu Glu Glu Glu Leu Glu Leu Asn Thr Gln Arg Ile Ser Ser Ser
 290 295 300
 Gln Ala Thr Gln Pro Leu Ala Thr Pro Val Val Ser Val Thr Thr Pro
 305 310 315 320
 Ser Leu Pro Pro Gln Gly Leu Val Tyr Ser Ala Met Pro Thr Ala Tyr
 325 330 335
 Asn Thr Asp Tyr Ser Leu Thr Ser Ala Asp Leu Ser Ala Leu Gln Gly
 340 345 350
 Phe Asn Ser Pro Gly Met Leu Ser Leu Gly Gln Val Ser Ala Trp Gln
 355 360 365
 Gln His His Leu Gly Gln Ala Ala Leu Ser Ser Leu Val Ala Gly Gly
 370 375 380
 Gln Leu Ser Gln Gly Ser Asn Leu Ser Ile Asn Thr Asn Gln Asn Ile
 385 390 395 400
 Ser Ile Lys Ser Glu Pro Ile Ser Pro Pro Arg Asp Arg Met Thr Pro
 405 410 415
 Ser Gly Phe Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro
 420 425 430
 Pro Pro Pro Gln Pro Gln Pro Gln Pro Pro Gln Pro Arg Gln

435 440 445
 Glu Met Gly Arg Ser Pro Val Asp Ser Leu Ser Ser Ser Ser Ser
 450 455 460
 Tyr Asp Gly Ser Asp Arg Glu Asp Pro Arg Gly Asp Phe His Ser Pro
 465 470 475 480
 Ile Val Leu Gly Arg Pro Pro Asn Thr Glu Asp Arg Glu Ser Pro Ser
 485 490 495
 Val Lys Arg Met Arg Met Asp Ala Trp Val Thr
 500 505

<210> 14

<211> 1521

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1524)

<400> 14

atg ggg cgg aag aaa ata caa atc aca cgc ata atg gat gaa agg aac 48
 Met Gly Arg Lys Lys Ile Gln Ile Thr Arg Ile Met Asp Glu Arg Asn
 1 5 10 15
 cga cag gtc act ttt aca aag aga aag ttt gga tta atg aag aaa gcc 96
 Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala
 20 25 30
 tat gaa ctt agt gtg ctc tgt gac tgt gaa ata gca ctc atc att ttc 144
 Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe
 35 40 45
 aac agc tct aac aaa ctg ttt caa tat gct agc act gat atg gac aaa 192
 Asn Ser Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys
 50 55 60
 gtt ctt ctc aag tat aca gaa tat aat gaa cct cat gaa agc aga acc 240
 Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr
 65 70 75 80
 aac tgc gat att gtt gag gct ctg aac aag aag gaa cac aga ggg tgc 288
 Asn Ser Asp Ile Val Glu Ala Leu Asn Lys Lys Glu His Arg Gly Cys
 85 90 95
 gac agc cca gac cct gat act tca tat gtg cta act cca cat aca gaa 336
 Asp Ser Pro Asp Pro Asp Thr Ser Tyr Val Leu Thr Pro His Thr Glu
 100 105 110
 gaa aaa tat aaa aaa att aat gag gaa ttt gat aat atg atg cgg aat 384
 Glu Lys Tyr Lys Lys Ile Asn Glu Glu Phe Asp Asn Met Met Arg Asn
 115 120 125
 cat aaa atc gca cct ggt ctg cca cct cag aac ttt tca atg tct gtc 432
 His Lys Ile Ala Pro Gly Leu Pro Pro Gln Asn Phe Ser Met Ser Val
 130 135 140
 aca gtt cca gtg acc agc ccc aat gct ttg tcc tac act aac cca ggg 480
 Thr Val Pro Val Thr Ser Pro Asn Ala Leu Ser Tyr Thr Asn Pro Gly

145 150 155 160
 agt tca ctg gtg tcc cca tct ttg gca gcc agc tca acg tta aca gat 528
 Ser Ser Leu Val Ser Pro Ser Leu Ala Ala Ser Ser Thr Leu Thr Asp
 165 170 175
 tca agc atg ctc tct cca cct caa acc aca tta cat aga aat gtg tct 576
 Ser Ser Met Leu Ser Pro Pro Gln Thr Thr Leu His Arg Asn Val Ser
 180 185 190
 cct gga gct cct cag aga cca cca agt act ggc aat gca ggt ggg atg 624
 Pro Gly Ala Pro Gln Arg Pro Pro Ser Thr Gly Asn Ala Gly Gly Met
 195 200 205
 ttg agc act aca gac ctc aca gtg cca aat gga gct gga agc agt cca 672
 Leu Ser Thr Thr Asp Leu Thr Val Pro Asn Gly Ala Gly Ser Ser Pro
 210 215 220
 gtg ggg aat gga ttt gta aac tca aga gct tct cca aat ttg att gga 720
 Val Gly Asn Gly Phe Val Asn Ser Arg Ala Ser Pro Asn Leu Ile Gly
 225 230 235 240
 gct act ggt gca aat agc tta ggc aaa gtc atg cct aca aag tct ccc 768
 Ala Thr Gly Ala Asn Ser Leu Gly Lys Val Met Pro Thr Lys Ser Pro
 245 250 255
 cct cca cca ggt ggt ggt aat ctt gga atg aac agt agg aaa cca gat 816
 Pro Pro Pro Gly Gly Gly Asn Leu Gly Met Asn Ser Arg Lys Pro Asp
 260 265 270
 ctt cga gtt gtc atc ccc cct tca agc aag ggc atg atg cct cca cta 864
 Leu Arg Val Val Ile Pro Pro Ser Ser Lys Gly Met Met Pro Pro Leu
 275 280 285
 tcg gag gaa gag gaa ttg gag ttg aac acc caa agg atc agt agt tct 912
 Ser Glu Glu Glu Glu Leu Glu Leu Asn Thr Gln Arg Ile Ser Ser Ser
 290 295 300
 caa gcc act caa cct ctt gct acc cca gtc gtg tct gtg aca acc cca 960
 Gln Ala Thr Gln Pro Leu Ala Thr Pro Val Val Ser Val Thr Thr Pro
 305 310 315 320
 agc ttg cct ccg caa gga ctt gtg tac tca gca atg ccg act gcc tac 1008
 Ser Leu Pro Pro Gln Gly Leu Val Tyr Ser Ala Met Pro Thr Ala Tyr
 325 330 335
 aac act gat tat tca ctg acc agc gct gac ctg tca gcc ctt caa ggc 1056
 Asn Thr Asp Tyr Ser Leu Thr Ser Ala Asp Leu Ser Ala Leu Gln Gly
 340 345 350
 ttc aac tcg cca gga atg ctg tcg ctg gga cag gtg tcg gcc tgg cag 1104
 Phe Asn Ser Pro Gly Met Leu Ser Leu Gly Gln Val Ser Ala Trp Gln
 355 360 365
 cag cac cac cta gga caa gca gcc ctc agc tct ctt gtt gct gga ggg 1152
 Gln His His Leu Gly Gln Ala Ala Leu Ser Ser Leu Val Ala Gly Gly
 370 375 380
 cag tta tct cag ggt tcc aat tta tcc att aat acc aac caa aac atc 1200
 Gln Leu Ser Gln Gly Ser Asn Leu Ser Ile Asn Thr Asn Gln Asn Ile
 385 390 395 400

agc atc aag tcc gaa ccg att tca cct cct cgg gat cgt atg acc cca 1248
 Ser Ile Lys Ser Glu Pro Ile Ser Pro Pro Arg Asp Arg Met Thr Pro
 405 410 415
 tcg ggc ttc cag cag cag cag cag cag cag cag cag cag ccg ccg 1296
 Ser Gly Phe Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro
 420 425 430
 cca cca ccg cag ccc cag cca caa ccc ccg cag ccc cag ccc cga cag 1344
 Pro Pro Pro Gln Pro Gln Pro Gln Pro Pro Gln Pro Gln Pro Arg Gln
 435 440 445
 gaa atg ggg cgc tcc cct gtg gac agt ctg agc agc tct agt agc tcc 1392
 Glu Met Gly Arg Ser Pro Val Asp Ser Leu Ser Ser Ser Ser Ser Ser
 450 455 460
 tat gat ggc agt gat cgg gag gat cca cgg ggc gac ttc cat tct cca 1440
 Tyr Asp Gly Ser Asp Arg Glu Asp Pro Arg Gly Asp Phe His Ser Pro
 465 470 475 480
 att gtg ctt ggc cga ccc cca aac act gag gac aga gaa agc cct tct 1488
 Ile Val Leu Gly Arg Pro Pro Asn Thr Glu Asp Arg Glu Ser Pro Ser
 485 490 495
 gta aag cga atg agg atg gac gcg tgg gtg acc 1521
 Val Lys Arg Met Arg Met Asp Ala Trp Val Thr
 500 505
 <210> 15
 <211> 365
 <212> PRT
 <213> Homo sapiens
 <400> 15
 Met Gly Arg Lys Lys Ile Gln Ile Ser Arg Ile Leu Asp Gln Arg Asn
 1 5 10 15
 Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala
 20 25 30
 Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe
 35 40 45
 Asn Ser Ala Asn Arg Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Arg
 50 55 60
 Val Leu Leu Lys Tyr Thr Glu Tyr Ser Glu Pro His Glu Ser Arg Thr
 65 70 75 80
 Asn Thr Asp Ile Leu Glu Thr Leu Lys Arg Arg Gly Ile Gly Leu Asp
 85 90 95
 Gly Pro Glu Leu Glu Pro Asp Glu Gly Pro Glu Glu Pro Gly Glu Lys
 100 105 110
 Phe Arg Arg Leu Ala Gly Glu Gly Gly Asp Pro Ala Leu Pro Arg Pro
 115 120 125
 Arg Leu Tyr Pro Ala Ala Pro Ala Met Pro Ser Pro Asp Val Val Tyr
 130 135 140
 Gly Ala Leu Pro Pro Pro Gly Cys Asp Pro Ser Gly Leu Gly Glu Ala
 145 150 155 160

Leu Pro Ala Gln Ser Arg Pro Ser Pro Phe Arg Pro Ala Ala Pro Lys
 165 170 175
 Ala Gly Pro Pro Gly Leu Val His Pro Leu Phe Ser Pro Ser His Leu
 180 185 190
 Thr Ser Lys Thr Pro Pro Pro Leu Tyr Leu Pro Thr Glu Gly Arg Arg
 195 200 205
 Ser Asp Leu Pro Gly Gly Leu Ala Gly Pro Arg Gly Gly Leu Asn Thr
 210 215 220
 Ser Arg Ser Leu Tyr Ser Gly Leu Gln Asn Pro Cys Ser Thr Ala Thr
 225 230 235 240
 Pro Gly Pro Pro Leu Gly Ser Phe Pro Phe Leu Pro Gly Gly Pro Pro
 245 250 255
 Val Gly Ala Glu Ala Trp Ala Arg Arg Val Pro Gln Pro Ala Ala Pro
 260 265 270
 Pro Arg Arg Pro Pro Gln Ser Ala Ser Ser Leu Ser Ala Ser Leu Arg
 275 280 285
 Pro Pro Gly Ala Pro Ala Thr Phe Leu Arg Pro Ser Pro Ile Pro Cys
 290 295 300
 Ser Ser Pro Gly Pro Trp Gln Ser Leu Cys Gly Leu Gly Pro Pro Cys
 305 310 315 320
 Ala Gly Cys Pro Trp Pro Thr Ala Gly Pro Gly Arg Arg Ser Pro Gly
 325 330 335
 Gly Thr Ser Pro Glu Arg Ser Pro Gly Thr Ala Arg Ala Arg Gly Asp
 340 345 350
 Pro Thr Ser Leu Gln Ala Ser Ser Glu Lys Thr Gln Gln
 355 360 365

<210> 16

<211> 1095

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1098)

<400> 16

atg ggg agg aaa aaa atc cag atc tcc cgc atc ctg gac caa agg aat 48
 Met Gly Arg Lys Lys Ile Gln Ile Ser Arg Ile Leu Asp Gln Arg Asn
 1 5 10 15
 cgg cag gtg acg ttc acc aag cgg aag ttc ggg ctg atg aag aag gcc 96
 Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala
 20 25 30
 tat gag ctg agc gtg ctc tgt gac tgt gag ata gcc ctc atc atc ttc 144
 Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe
 35 40 45
 aac agc gcc aac cgc ctc ttc cag tat gcc agc acg gac atg gac cgt 192
 Asn Ser Ala Asn Arg Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Arg
 50 55 60

gtg ctg ctg aag tac aca gag tac agc gag ccc cac gag agc cgc acc 240
 Val Leu Leu Lys Tyr Thr Glu Tyr Ser Glu Pro His Glu Ser Arg Thr
 65 70 75 80
 aac act gac atc ctc gag acg ctg aag cgg agg ggc att ggc ctc gat 288
 Asn Thr Asp Ile Leu Glu Thr Leu Lys Arg Arg Gly Ile Gly Leu Asp
 85 90 95
 ggg cca gag ctg gag ccg gat gaa ggg cct gag gag cca gga gag aag 336
 Gly Pro Glu Leu Glu Pro Asp Glu Gly Pro Glu Glu Pro Gly Glu Lys
 100 105 110
 ttt cgg agg ctg gca ggc gaa ggg ggt gat ccg gcc ttg ccc cga ccc 384
 Phe Arg Arg Leu Ala Gly Glu Gly Gly Asp Pro Ala Leu Pro Arg Pro
 115 120 125
 cgg ctg tat cct gca gct cct gct atg ccc agc cca gat gtg gta tac 432
 Arg Leu Tyr Pro Ala Ala Pro Ala Met Pro Ser Pro Asp Val Val Tyr
 130 135 140
 ggg gcc tta ccg cca cca ggc tgt gac ccc agt ggg ctt ggg gaa gca 480
 Gly Ala Leu Pro Pro Gly Cys Asp Pro Ser Gly Leu Gly Glu Ala
 145 150 155 160
 ctg ccc gcc cag agc cgc cca tct ccc ttc cga cca gca gcc ccc aaa 528
 Leu Pro Ala Gln Ser Arg Pro Ser Pro Phe Arg Pro Ala Ala Pro Lys
 165 170 175
 gcc ggg ccc cca ggc ctg gtg cac cct ctc ttc tca cca agc cac ctc 576
 Ala Gly Pro Pro Gly Leu Val His Pro Leu Phe Ser Pro Ser His Leu
 180 185 190
 acc agc aag aca cca ccc cca ctg tac ctg ccg acg gaa ggg cgg agg 624
 Thr Ser Lys Thr Pro Pro Pro Leu Tyr Leu Pro Thr Glu Gly Arg Arg
 195 200 205
 tca gac ctg cct ggt ggc ctg gct ggg ccc cga ggg gga cta aac acc 672
 Ser Asp Leu Pro Gly Gly Leu Ala Gly Pro Arg Gly Gly Leu Asn Thr
 210 215 220
 tcc aga agc ctc tac agt ggc ctg cag aac ccc tgc tcc act gca act 720
 Ser Arg Ser Leu Tyr Ser Gly Leu Gln Asn Pro Cys Ser Thr Ala Thr
 225 230 235 240
 ccc gga ccc cca ctg ggg agc ttc ccc ttc ctc ccc gga ggc ccc cca 768
 Pro Gly Pro Pro Leu Gly Ser Phe Pro Phe Leu Pro Gly Gly Pro Pro
 245 250 255
 gtg ggg gcc gaa gcc tgg gcg agg agg gtc ccc caa ccc gcg gcg cct 816
 Val Gly Ala Glu Ala Trp Ala Arg Arg Val Pro Gln Pro Ala Ala Pro
 260 265 270
 ccc cgc cga ccc ccc cag tca gca tca agt ctg agc gcc tct ctc cgg 864
 Pro Arg Arg Pro Pro Gln Ser Ala Ser Ser Leu Ser Ala Ser Leu Arg
 275 280 285
 ccc ccg ggg gcc ccg gcg act ttc cta aga cct tcc cct atc cct tgc 912
 Pro Pro Gly Ala Pro Ala Thr Phe Leu Arg Pro Ser Pro Ile Pro Cys
 290 295 300
 tcc tcg ccc ggt ccc tgg cag agc ctc tgc ggc ctg ggc ccg ccc tgc 960

Ser Ser Pro Gly Pro Trp Gln Ser Leu Cys Gly Leu Gly Pro Pro Cys
 305 310 315 320
 gcc ggc tgc cct tgg ccg acg gct ggc ccc ggt agg aga tca ccc ggt 1008
 Ala Gly Cys Pro Trp Pro Thr Ala Gly Pro Gly Arg Arg Ser Pro Gly
 325 330 335
 ggc acc agc cca gag cgc tcg cca ggt acg gcg agg gca cgt ggg gac 1056
 Gly Thr Ser Pro Glu Arg Ser Pro Gly Thr Ala Arg Ala Arg Gly Asp
 340 345 350
 ccc acc tcc ctc cag gcc tct tca gag aag acc caa cag 1095
 Pro Thr Ser Leu Gln Ala Ser Ser Glu Lys Thr Gln Gln
 355 360 365
 <210> 17
 <211> 465
 <212> PRT
 <213> Homo sapiens
 <400> 17
 Met Gly Arg Lys Lys Ile Gln Ile Thr Arg Ile Met Asp Glu Arg Asn
 1 5 10 15
 Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala
 20 25 30
 Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe
 35 40 45
 Asn Ser Thr Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys
 50 55 60
 Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr
 65 70 75 80
 Asn Ser Asp Ile Val Glu Thr Leu Arg Lys Lys Gly Leu Asn Gly Cys
 85 90 95
 Asp Ser Pro Asp Pro Asp Ala Asp Asp Ser Val Gly His Ser Pro Glu
 100 105 110
 Ser Glu Asp Lys Tyr Arg Lys Ile Asn Glu Asp Ile Asp Leu Met Ile
 115 120 125
 Ser Arg Gln Arg Leu Cys Ala Val Pro Pro Pro Asn Phe Glu Met Pro
 130 135 140
 Val Ser Ile Pro Val Ser Ser His Asn Ser Leu Val Tyr Ser Asn Pro
 145 150 155 160
 Val Ser Ser Leu Gly Asn Pro Asn Leu Leu Pro Leu Ala His Pro Ser
 165 170 175
 Leu Gln Arg Asn Ser Met Ser Pro Gly Val Thr His Arg Pro Pro Ser
 180 185 190
 Ala Gly Asn Thr Gly Gly Leu Met Gly Gly Asp Leu Thr Ser Gly Ala
 195 200 205
 Gly Thr Ser Ala Gly Asn Gly Tyr Gly Asn Pro Arg Asn Ser Pro Gly
 210 215 220
 Leu Leu Val Ser Pro Gly Asn Leu Asn Lys Asn Met Gln Ala Lys Ser
 225 230 235 240

Pro Pro Pro Met Asn Leu Gly Met Asn Asn Arg Lys Pro Asp Leu Arg
 245 250 255
 Val Leu Ile Pro Pro Gly Ser Lys Asn Thr Met Pro Ser Val Asn Gln
 260 265 270
 Arg Ile Asn Asn Ser Gln Ser Ala Gln Ser Leu Ala Thr Pro Val Val
 275 280 285
 Ser Val Ala Thr Pro Thr Leu Pro Gly Gln Gly Met Gly Gly Tyr Pro
 290 295 300
 Ser Ala Ile Ser Thr Thr Tyr Gly Thr Glu Tyr Ser Leu Ser Ser Ala
 305 310 315 320
 Asp Leu Ser Ser Leu Ser Gly Phe Asn Thr Ala Ser Ala Leu His Leu
 325 330 335
 Gly Ser Val Thr Gly Trp Gln Gln Gln His Leu His Asn Met Pro Pro
 340 345 350
 Ser Ala Leu Ser Gln Leu Gly Ala Cys Thr Ser Thr His Leu Ser Gln
 355 360 365
 Ser Ser Asn Leu Ser Leu Pro Ser Thr Gln Ser Leu Asn Ile Lys Ser
 370 375 380
 Glu Pro Val Ser Pro Pro Arg Asp Arg Thr Thr Thr Pro Ser Arg Tyr
 385 390 395 400
 Pro Gln His Thr Arg His Glu Ala Gly Arg Ser Pro Val Asp Ser Leu
 405 410 415
 Ser Ser Cys Ser Ser Ser Tyr Asp Gly Ser Asp Arg Glu Asp His Arg
 420 425 430
 Asn Glu Phe His Ser Pro Ile Gly Leu Thr Arg Pro Ser Pro Asp Glu
 435 440 445
 Arg Glu Ser Pro Ser Val Lys Arg Met Arg Leu Ser Glu Gly Trp Ala
 450 455 460

Thr

<210> 18

<211> 1395

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1398)

<400> 18

atg ggg aga aaa aag att cag att acg agg att atg gat gaa cgt aac 48

Met Gly Arg Lys Lys Ile Gln Ile Thr Arg Ile Met Asp Glu Arg Asn

1 5 10 15

aga cag gtg aca ttt aca aag agg aaa ttt ggg ttg atg aag aag gct 96

Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala

20 25 30

tat gag ctg agc gtg ctg tgt gac tgt gag att gcg ctg atc atc ttc 144

Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe

35 40 45

aac agc acc aac aag ctg ttc cag tat gcc agc acc gac atg gac aaa 192
 Asn Ser Thr Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys
 50 55 60
 gtg ctt ctc aag tac acg gag tac aac gag ccg cat gag agc cgg aca 240
 Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr
 65 70 75 80
 aac tca gac atc gtg gag acg ttg aga aag aag ggc ctt aat ggc tgt 288
 Asn Ser Asp Ile Val Glu Thr Leu Arg Lys Lys Gly Leu Asn Gly Cys
 85 90 95
 gac agc cca gac ccc gat gcg gac gat tcc gta ggt cac agc cct gag 336
 Asp Ser Pro Asp Pro Asp Ala Asp Asp Ser Val Gly His Ser Pro Glu
 100 105 110
 tct gag gac aag tac agg aaa att aac gaa gat att gat cta atg atc 384
 Ser Glu Asp Lys Tyr Arg Lys Ile Asn Glu Asp Ile Asp Leu Met Ile
 115 120 125
 agc agg caa aga ttg tgt gct gtt cca cct ccc aac ttc gag atg cca 432
 Ser Arg Gln Arg Leu Cys Ala Val Pro Pro Pro Asn Phe Glu Met Pro
 130 135 140
 gtc tcc atc cca gtg tcc agc cac aac agt ttg gtg tac agc aac cct 480
 Val Ser Ile Pro Val Ser Ser His Asn Ser Leu Val Tyr Ser Asn Pro
 145 150 155 160
 gtc agc tca ctg gga aac ccc aac cta ttg cca ctg gct cac cct tct 528
 Val Ser Ser Leu Gly Asn Pro Asn Leu Leu Pro Leu Ala His Pro Ser
 165 170 175
 ctg cag agg aat agt atg tct cct ggt gta aca cat cga cct cca agt 576
 Leu Gln Arg Asn Ser Met Ser Pro Gly Val Thr His Arg Pro Pro Ser
 180 185 190
 gca ggt aac aca ggt ggt ctg atg ggt gga gac ctc acg tct ggt gca 624
 Ala Gly Asn Thr Gly Gly Leu Met Gly Gly Asp Leu Thr Ser Gly Ala
 195 200 205
 ggc acc agt gca ggg aac ggg tat ggc aat ccc cga aac tca cca ggt 672
 Gly Thr Ser Ala Gly Asn Gly Tyr Gly Asn Pro Arg Asn Ser Pro Gly
 210 215 220
 ctg ctg gtc tca cct ggt aac ttg aac aag aat atg caa gca aaa tct 720
 Leu Leu Val Ser Pro Gly Asn Leu Asn Lys Asn Met Gln Ala Lys Ser
 225 230 235 240
 cct ccc cca atg aat tta gga atg aat aac cgt aaa cca gat ctc cga 768
 Pro Pro Pro Met Asn Leu Gly Met Asn Asn Arg Lys Pro Asp Leu Arg
 245 250 255
 gtt ctt att cca cca ggc agc aag aat acg atg cca tca gtg aat caa 816
 Val Leu Ile Pro Pro Gly Ser Lys Asn Thr Met Pro Ser Val Asn Gln
 260 265 270
 agg ata aat aac tcc cag tcg gct cag tca ttg gct acc cca gtg gtt 864
 Arg Ile Asn Asn Ser Gln Ser Ala Gln Ser Leu Ala Thr Pro Val Val
 275 280 285
 tcc gta gca act cct act tta cca gga caa gga atg gga gga tat cca 912

Ser Val Ala Thr Pro Thr Leu Pro Gly Gln Gly Met Gly Gly Tyr Pro
 290 295 300
 tca gcc att tca aca aca tat ggt acc gag tac tct ctg agt agt gca 960
 Ser Ala Ile Ser Thr Thr Tyr Gly Thr Glu Tyr Ser Leu Ser Ser Ala
 305 310 315 320
 gac ctg tca tct ctg tct ggg ttt aac acc gcc agc gct ctt cac ctt 1008
 Asp Leu Ser Ser Leu Ser Gly Phe Asn Thr Ala Ser Ala Leu His Leu
 325 330 335
 ggt tca gta act ggc tgg caa gag caa cac cta cat aac atg cca cca 1056
 Gly Ser Val Thr Gly Trp Gln Gln Gln His Leu His Asn Met Pro Pro
 340 345 350
 tct gcc ctc agt cag ttg gga gct tgc act agc act cat tta tct cag 1104
 Ser Ala Leu Ser Gln Leu Gly Ala Cys Thr Ser Thr His Leu Ser Gln
 355 360 365
 agt tca aat ctc tcc ctg cct tct act caa agc ctc aac atc aag tca 1152
 Ser Ser Asn Leu Ser Leu Pro Ser Thr Gln Ser Leu Asn Ile Lys Ser
 370 375 380
 gaa cct gtt tct cct cct aga gac cgt acc acc acc cct tcg aga tac 1200
 Glu Pro Val Ser Pro Pro Arg Asp Arg Thr Thr Thr Pro Ser Arg Tyr
 385 390 395 400
 cca caa cac acg cgc cac gag gcg ggg aga tct cct gtt gac agc ttg 1248
 Pro Gln His Thr Arg His Glu Ala Gly Arg Ser Pro Val Asp Ser Leu
 405 410 415
 agc agc tgt agc agt tcg tac gac ggg agc gac cga gag gat cac cgg 1296
 Ser Ser Cys Ser Ser Ser Tyr Asp Gly Ser Asp Arg Glu Asp His Arg
 420 425 430
 aac gaa ttc cac tcc ccc att gga ctc acc aga cct tcg ccg gac gaa 1344
 Asn Glu Phe His Ser Pro Ile Gly Leu Thr Arg Pro Ser Pro Asp Glu
 435 440 445
 agg gaa agt ccc tca gtc aag cgc atg cga ctt tct gaa gga tgg gca 1392
 Arg Glu Ser Pro Ser Val Lys Arg Met Arg Leu Ser Glu Gly Trp Ala
 450 455 460
 aca 1395
 Thr
 465
 <210> 19
 <211> 521
 <212> PRT
 <213> Homo sapiens
 <400> 19
 Met Gly Arg Lys Lys Ile Gln Ile Gln Arg Ile Thr Asp Glu Arg Asn
 1 5 10 15
 Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala
 20 25 30
 Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe
 35 40 45

Asn His Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys
 50 55 60
 Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr
 65 70 75 80
 Asn Ala Asp Ile Ile Glu Thr Leu Arg Lys Lys Gly Phe Asn Gly Cys
 85 90 95
 Asp Ser Pro Glu Pro Asp Gly Glu Asp Ser Leu Glu Gln Ser Pro Leu
 100 105 110
 Leu Glu Asp Lys Tyr Arg Arg Ala Ser Glu Glu Leu Asp Gly Leu Phe
 115 120 125
 Arg Arg Tyr Gly Ser Thr Val Pro Ala Pro Asn Phe Ala Met Pro Val
 130 135 140
 Thr Val Pro Val Ser Asn Gln Ser Ser Leu Gln Phe Ser Asn Pro Ser
 145 150 155 160
 Gly Ser Leu Val Thr Pro Ser Leu Val Thr Ser Ser Leu Thr Asp Pro
 165 170 175
 Arg Leu Leu Ser Pro Gln Gln Pro Ala Leu Gln Arg Asn Ser Val Ser
 180 185 190
 Pro Gly Leu Pro Gln Arg Pro Ala Ser Ala Gly Ala Met Leu Gly Gly
 195 200 205
 Asp Leu Asn Ser Ala Asn Gly Ala Cys Pro Ser Pro Val Gly Asn Gly
 210 215 220
 Tyr Val Ser Ala Arg Ala Ser Pro Gly Leu Leu Pro Val Ala Asn Gly
 225 230 235 240
 Asn Ser Leu Asn Lys Val Ile Pro Ala Lys Ser Pro Pro Pro Pro Thr
 245 250 255
 His Ser Thr Gln Leu Gly Ala Pro Ser Arg Lys Pro Asp Leu Arg Val
 260 265 270
 Ile Thr Ser Gln Ala Gly Lys Gly Leu Met His His Leu Thr Glu Asp
 275 280 285
 His Leu Asp Leu Asn Asn Ala Gln Arg Leu Gly Val Ser Gln Ser Thr
 290 295 300
 His Ser Leu Thr Thr Pro Val Val Ser Val Ala Thr Pro Ser Leu Leu
 305 310 315 320
 Ser Gln Gly Leu Pro Phe Ser Ser Met Pro Thr Ala Tyr Asn Thr Asp
 325 330 335
 Tyr Gln Leu Thr Ser Ala Glu Leu Ser Ser Ser Leu Pro Ala Phe Ser Ser
 340 345 350
 Pro Gly Gly Leu Ser Leu Gly Asn Val Thr Ala Trp Gln Gln Pro Gln
 355 360 365
 Gln Pro Gln Gln Pro Gln Gln Pro Gln Pro Pro Gln Gln Gln Pro Pro
 370 375 380
 Gln Pro Gln Gln Pro Gln Pro Gln Gln Pro Gln Gln Pro Gln Gln Pro
 385 390 395 400
 Pro Gln Gln Gln Ser His Leu Val Pro Val Ser Leu Ser Asn Leu Ile
 405 410 415

Pro Gly Ser Pro Leu Pro His Val Gly Ala Ala Leu Thr Val Thr Thr
 420 425 430
 His Pro His Ile Ser Ile Lys Ser Glu Pro Val Ser Pro Ser Arg Glu
 435 440 445
 Arg Ser Pro Ala Pro Pro Pro Pro Ala Val Phe Pro Ala Ala Arg Pro
 450 455 460
 Glu Pro Gly Asp Gly Leu Ser Ser Pro Ala Gly Gly Ser Tyr Glu Thr
 465 470 475 480
 Gly Asp Arg Asp Asp Gly Arg Gly Asp Phe Gly Pro Thr Leu Gly Leu
 485 490 495
 Leu Arg Pro Ala Pro Glu Pro Glu Ala Glu Gly Ser Ala Val Lys Arg
 500 505 510
 Met Arg Leu Asp Thr Trp Thr Leu Lys
 515 520

<210> 20
 <211> 1563
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <223> (1)..(1566)
 <400> 20

atg ggg agg aaa aag att cag atc cag cga atc acc gac gag cgg aac 48
 Met Gly Arg Lys Lys Ile Gln Ile Gln Arg Ile Thr Asp Glu Arg Asn
 1 5 10 15
 cga cag gtg act ttc acc aag cgg aag ttt ggc ctg atg aag aag gcg 96
 Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala
 20 25 30
 tat gag ctg agc gtg cta tgt gac tgc gag atc gca ctc atc atc ttc 144
 Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe
 35 40 45
 aac cac tcc aac aag ctg ttc cag tac gcc agc acc gac atg gac aag 192
 Asn His Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys
 50 55 60
 gtg ctg ctc aag tac acg gag tac aat gag cca cac gag agc cgc acc 240
 Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr
 65 70 75 80
 aac gcc gac atc atc gag acc ctg agg aag aag ggc ttc aat ggc tgc 288
 Asn Ala Asp Ile Ile Glu Thr Leu Arg Lys Lys Gly Phe Asn Gly Cys
 85 90 95
 gac agc ccc gag ccc gag ggg gag gac tgc ctg gaa cag agc ccc ctg 336
 Asp Ser Pro Glu Pro Asp Gly Glu Asp Ser Leu Glu Gln Ser Pro Leu
 100 105 110
 ctg gag gac aag tac cga cgc gcc agc gag gag ctc gac ggg ctc ttc 384
 Leu Glu Asp Lys Tyr Arg Arg Ala Ser Glu Glu Leu Asp Gly Leu Phe
 115 120 125

cgg cgc tat ggg tca act gtc ccg gcc ccc aac ttt gcc atg cct gtc 432
 Arg Arg Tyr Gly Ser Thr Val Pro Ala Pro Asn Phe Ala Met Pro Val
 130 135 140
 acg gtg ccc gtg tcc aat cag agc tca ctg cag ttc agc aat ccc agc 480
 Thr Val Pro Val Ser Asn Gln Ser Ser Leu Gln Phe Ser Asn Pro Ser
 145 150 155 160
 ggc tcc ctg gtc acc cct tcc ctg gtg aca tca tcc ctc acg gac ccg 528
 Gly Ser Leu Val Thr Pro Ser Leu Val Thr Ser Ser Leu Thr Asp Pro
 165 170 175
 cgg ctc ctg tcc ccc cag cag cca gca cta cag agg aac agt gtg tct 576
 Arg Leu Leu Ser Pro Gln Gln Pro Ala Leu Gln Arg Asn Ser Val Ser
 180 185 190
 cct ggc ctg ccc cag cgg cca gct agt gcg ggg gcc atg ctg ggg ggt 624
 Pro Gly Leu Pro Gln Arg Pro Ala Ser Ala Gly Ala Met Leu Gly Gly
 195 200 205
 gac ctg aac agt gct aac gga gcc tgc ccc agc cct gtt ggg aat ggc 672
 Asp Leu Asn Ser Ala Asn Gly Ala Cys Pro Ser Pro Val Gly Asn Gly
 210 215 220
 tac gtc agt gct cgg gct tcc cct ggc ctc ctc cct gtg gcc aat ggc 720
 Tyr Val Ser Ala Arg Ala Ser Pro Gly Leu Leu Pro Val Ala Asn Gly
 225 230 235 240
 aac agc cta aac aag gtc atc cct gcc aag tct ccg ccc cca cct acc 768
 Asn Ser Leu Asn Lys Val Ile Pro Ala Lys Ser Pro Pro Pro Thr
 245 250 255
 cac agc acc cag ctt gga gcc ccc agc cgc aag ccc gac ctg cga gtc 816
 His Ser Thr Gln Leu Gly Ala Pro Ser Arg Lys Pro Asp Leu Arg Val
 260 265 270
 atc act tcc cag gca gga aag ggg tta atg cat cac ttg act gag gac 864
 Ile Thr Ser Gln Ala Gly Lys Gly Leu Met His His Leu Thr Glu Asp
 275 280 285
 cat tta gat ctg aac aat gcc cag cgc ctt ggg gtc tcc cag tct act 912
 His Leu Asp Leu Asn Asn Ala Gln Arg Leu Gly Val Ser Gln Ser Thr
 290 295 300
 cat tcg ctc acc acc cca gtg gtt tct gtg gca acg ccg agt tta ctc 960
 His Ser Leu Thr Thr Pro Val Val Ser Val Ala Thr Pro Ser Leu Leu
 305 310 315 320
 agc cag ggc ctc ccc ttc tct tcc atg ccc act gcc tac aac aca gat 1008
 Ser Gln Gly Leu Pro Phe Ser Ser Met Pro Thr Ala Tyr Asn Thr Asp
 325 330 335
 tac cag ttg acc agt gca gag ctc tcc tcc tta cca gcc ttt agt tca 1056
 Tyr Gln Leu Thr Ser Ala Glu Leu Ser Ser Leu Pro Ala Phe Ser Ser
 340 345 350
 cct ggg ggg ctg tcg cta ggc aat gtc act gcc tgg caa cag cca cag 1104
 Pro Gly Gly Leu Ser Leu Gly Asn Val Thr Ala Trp Gln Gln Pro Gln
 355 360 365
 cag ccc cag cag ccg cag cag cca cag cct cca cag cag cca ccg 1152

Gln Pro Gln Gln Pro Gln Gln Pro Gln Pro Pro Gln Gln Gln Pro Pro
 370 375 380
 cag cca cag cag cca cag cca cag cag cct cag cag ccg caa cag cca 1200
 Gln Pro Gln Gln Pro Gln Pro Gln Gln Pro Gln Gln Pro Gln Gln Pro
 385 390 395 400
 cct cag caa cag tcc cac ctg gtc cct gta tct ctc agc aac ctc atc 1248
 Pro Gln Gln Gln Ser His Leu Val Pro Val Ser Leu Ser Asn Leu Ile
 405 410 415
 ccg ggc agc ccc ctg ccc cac gtg ggt gct gcc ctc aca gtc acc acc 1296
 Pro Gly Ser Pro Leu Pro His Val Gly Ala Ala Leu Thr Val Thr Thr
 420 425 430
 cac ccc cac atc agc atc aag tca gaa ccg gtg tcc cca agc cgt gag 1344
 His Pro His Ile Ser Ile Lys Ser Glu Pro Val Ser Pro Ser Arg Glu
 435 440 445
 cgc agc cct gcg cct ccc cct cca gct gtg ttc cca gct gcc cgc cct 1392
 Arg Ser Pro Ala Pro Pro Pro Pro Ala Val Phe Pro Ala Ala Arg Pro
 450 455 460
 gag cct ggc gat ggt ctc agc agc cca gcc ggg gga tcc tat gag acg 1440
 Glu Pro Gly Asp Gly Leu Ser Ser Pro Ala Gly Gly Ser Tyr Glu Thr
 465 470 475 480
 gga gac cgg gat gac gga cgg ggg gac ttc ggg ccc aca ctg ggc ctg 1488
 Gly Asp Arg Asp Asp Gly Arg Gly Asp Phe Gly Pro Thr Leu Gly Leu
 485 490 495
 ctg cgc cca gcc cca gag cct gag gct gag ggc tca gct gtg aag agg 1536
 Leu Arg Pro Ala Pro Glu Pro Glu Ala Glu Gly Ser Ala Val Lys Arg
 500 505 510
 atg cgg ctt gat acc tgg aca tta aag 1563
 Met Arg Leu Asp Thr Trp Thr Leu Lys
 515 520
 <210> 21
 <211> 217
 <212> PRT
 <213> Rattus norvegicus
 <400> 21
 Met Ser Leu Val Gly Gly Phe Pro His His Pro Val Val His His Glu
 1 5 10 15
 Gly Tyr Pro Phe Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala
 20 25 30
 Ser Arg Cys Ser His Glu Glu Asn Pro Tyr Phe His Gly Trp Leu Ile
 35 40 45
 Gly His Pro Glu Met Ser Pro Pro Asp Tyr Ser Met Ala Leu Ser Tyr
 50 55 60
 Ser Pro Glu Tyr Ala Ser Gly Ala Ala Gly Leu Asp His Ser His Tyr
 65 70 75 80
 Gly Gly Val Pro Pro Gly Ala Gly Pro Pro Gly Leu Gly Gly Pro Arg
 85 90 95

Pro Val Lys Arg Arg Gly Thr Ala Asn Arg Lys Glu Arg Arg Arg Thr
 100 105 110
 Gln Ser Ile Asn Ser Ala Phe Ala Glu Leu Arg Glu Cys Ile Pro Asn
 115 120 125
 Val Pro Ala Asp Thr Lys Leu Ser Lys Ile Lys Thr Leu Arg Leu Ala
 130 135 140
 Thr Ser Tyr Ile Ala Tyr Leu Met Asp Leu Leu Ala Lys Asp Asp Gln
 145 150 155 160
 Asn Gly Glu Ala Glu Ala Phe Lys Ala Glu Ile Lys Lys Thr Asp Val
 165 170 175
 Lys Glu Glu Lys Arg Lys Lys Glu Leu Asn Glu Ile Leu Lys Ser Thr
 180 185 190
 Val Ser Ser Asn Asp Lys Lys Thr Lys Gly Arg Thr Gly Trp Pro Gln
 195 200 205
 His Val Trp Ala Leu Glu Leu Lys Gln
 210 215

<210> 22

<211> 651

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<223> (1)..(654)

<400> 22

atg agt ctg gtg ggg ggc ttt ccc cac cac ccc gtg gtg cac cat gag 48
 Met Ser Leu Val Gly Gly Phe Pro His His Pro Val Val His His Glu
 1 5 10 15
 ggc tac ccg ttc gcc gca gcc gca gcc gcc gct gct gct gcc gcc gcc 96
 Gly Tyr Pro Phe Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala
 20 25 30
 agc cgc tgc agt cac gag gag aac ccc tat ttc cac ggc tgg ctt att 144
 Ser Arg Cys Ser His Glu Glu Asn Pro Tyr Phe His Gly Trp Leu Ile
 35 40 45
 ggc cac ccg gag atg tgc ccc ccc gac tac agc atg gcc ctg tcc tac 192
 Gly His Pro Glu Met Ser Pro Pro Asp Tyr Ser Met Ala Leu Ser Tyr
 50 55 60
 agt ccc gag tac gcc agc ggt gcc ggc ggc ctg gac cac tcc cat tat 240
 Ser Pro Glu Tyr Ala Ser Gly Ala Ala Gly Leu Asp His Ser His Tyr
 65 70 75 80
 ggg gga gtg ccg ccc ggt gcc ggg cct ccc ggc ctg ggg ggg cgg cgc 288
 Gly Gly Val Pro Pro Gly Ala Gly Pro Pro Gly Leu Gly Gly Pro Arg
 85 90 95
 ccg gtg aag cgt cgg ggc acc gcc aac cgc aag gag cgg cgc agg act 336
 Pro Val Lys Arg Arg Gly Thr Ala Asn Arg Lys Glu Arg Arg Arg Thr
 100 105 110
 cag agc atc aac agc gcc ttc gcc gag ctg cgc gag tgc atc ccc aac 384

Gln Ser Ile Asn Ser Ala Phe Ala Glu Leu Arg Glu Cys Ile Pro Asn
 115 120 125
 gtg ccc gcc gac acc aaa ctc tcc aaa atc aag act ctg cgc ctg gcc 432
 Val Pro Ala Asp Thr Lys Leu Ser Lys Ile Lys Thr Leu Arg Leu Ala
 130 135 140
 acc agc tac atc gcc tac ctc atg gat ctg ctg gcc aag gac gac cag 480
 Thr Ser Tyr Ile Ala Tyr Leu Met Asp Leu Leu Ala Lys Asp Asp Gln
 145 150 155 160
 aac gga gag gcg gag gcc ttc aag gcg gag atc aag aag acc gac gtg 528
 Asn Gly Glu Ala Glu Ala Phe Lys Ala Glu Ile Lys Lys Thr Asp Val
 165 170 175
 aaa gag gag aag agg aag aaa gag ctg aat gaa atc ttg aaa agt aca 576
 Lys Glu Glu Lys Arg Lys Lys Glu Leu Asn Glu Ile Leu Lys Ser Thr
 180 185 190
 gtg agc agc aac gac aag aaa acc aaa ggc cgg aca ggc tgg cca cag 624
 Val Ser Ser Asn Asp Lys Lys Thr Lys Gly Arg Thr Gly Trp Pro Gln
 195 200 205
 cac gtc tgg gcc ctg gag ctc aag cag 651
 His Val Trp Ala Leu Glu Leu Lys Gln
 210 215
 <210> 23
 <211> 215
 <212> PRT
 <213> Homo sapiens
 <400> 23
 Met Asn Leu Val Gly Ser Tyr Ala His His His His His His Pro
 1 5 10 15
 His Pro Ala His Pro Met Leu His Glu Pro Phe Leu Phe Gly Pro Ala
 20 25 30
 Ser Arg Cys His Gln Glu Arg Pro Tyr Phe Gln Ser Trp Leu Leu Ser
 35 40 45
 Pro Ala Asp Ala Ala Pro Asp Phe Pro Ala Gly Gly Pro Pro Pro Ala
 50 55 60
 Ala Ala Ala Ala Ala Thr Ala Tyr Gly Pro Asp Ala Arg Pro Gly Gln
 65 70 75 80
 Ser Pro Gly Arg Leu Glu Ala Leu Gly Gly Arg Leu Gly Arg Arg Lys
 85 90 95
 Gly Ser Gly Pro Lys Lys Glu Arg Arg Gly Thr Glu Ser Ile Asn Ser
 100 105 110
 Ala Phe Ala Glu Leu Arg Glu Cys Ile Pro Asn Val Pro Ala Asp Thr
 115 120 125
 Lys Leu Ser Lys Ile Lys Thr Leu Arg Leu Ala Thr Ser Tyr Ile Ala
 130 135 140
 Tyr Leu Met Asp Val Leu Ala Lys Asp Ala Gln Ser Gly Asp Pro Glu
 145 150 155 160
 Ala Phe Lys Ala Glu Leu Lys Lys Ala Asp Gly Gly Arg Glu Ser Lys

165 170 175
 Arg Lys Arg Glu Leu Gln Gln His Glu Gly Phe Pro Pro Ala Leu Gly
 180 185 190
 Pro Val Glu Lys Arg Ile Lys Gly Arg Thr Gly Trp Pro Gln Gln Val
 195 200 205
 Trp Ala Leu Glu Leu Asn Gln
 210 215
 <210> 24
 <211> 645
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <223> (1)..(648)
 <400> 24
 atg aac ctc gtg ggc agc tac gca cac cat cac cac cat cac cac ccg 48
 Met Asn Leu Val Gly Ser Tyr Ala His His His His His His His Pro
 1 5 10 15
 cac cct gcg cac ccc atg ctc cac gaa ccc ttc ctc ttc ggt ccg gcc 96
 His Pro Ala His Pro Met Leu His Glu Pro Phe Leu Phe Gly Pro Ala
 20 25 30
 tcg cgc tgt cat cag gaa agg ccc tac ttc cag agc tgg ctg ctg agc 144
 Ser Arg Cys His Gln Glu Arg Pro Tyr Phe Gln Ser Trp Leu Leu Ser
 35 40 45
 ccg gct gac gct gcc ccg gac ttc cct gcg ggc ggg ccg ccg ccc gcg 192
 Pro Ala Asp Ala Ala Pro Asp Phe Pro Ala Gly Gly Pro Pro Pro Ala
 50 55 60
 gcc gct gca gcc gcc acc gcc tat ggt cct gac gcc agg cct ggg cag 240
 Ala Ala Ala Ala Ala Thr Ala Tyr Gly Pro Asp Ala Arg Pro Gly Gln
 65 70 75 80
 agc ccc ggg cgg ctg gag gcg ctt ggc ggc cgt ctt ggc cgg cgg aaa 288
 Ser Pro Gly Arg Leu Glu Ala Leu Gly Gly Arg Leu Gly Arg Arg Lys
 85 90 95
 ggc tca gga ccc aag aag gag cgg aga cgc act gag agc att aac agc 336
 Gly Ser Gly Pro Lys Lys Glu Arg Arg Arg Thr Glu Ser Ile Asn Ser
 100 105 110
 gca ttc gcg gag ttg cgc gag tgc atc ccc aac gtg ccg gcc gac acc 384
 Ala Phe Ala Glu Leu Arg Glu Cys Ile Pro Asn Val Pro Ala Asp Thr
 115 120 125
 aag ctc tcc aag atc aag act ctg cgc cta gcc acc agc tac atc gcc 432
 Lys Leu Ser Lys Ile Lys Thr Leu Arg Leu Ala Thr Ser Tyr Ile Ala
 130 135 140
 tac ctg atg gac gtg ctg gcc aag gat gca cag tct ggc gat ccc gag 480
 Tyr Leu Met Asp Val Leu Ala Lys Asp Ala Gln Ser Gly Asp Pro Glu
 145 150 155 160
 gcc ttc aag gct gaa ctc aag aag gcg gat ggc ggc cgt gag agc aag 528

Ala Phe Lys Ala Glu Leu Lys Lys Ala Asp Gly Gly Arg Glu Ser Lys
 165 170 175
 cgg aaa agg gag ctg cag cag cac gaa ggt ttt cct cct gcc ctg ggc 576
 Arg Lys Arg Glu Leu Gln Gln His Glu Gly Phe Pro Pro Ala Leu Gly
 180 185 190
 cca gtc gag aag agg att aaa gga cgc acc ggc tgg ccg cag caa gtc 624
 Pro Val Glu Lys Arg Ile Lys Gly Arg Thr Gly Trp Pro Gln Gln Val
 195 200 205
 tgg gcg ctg gag tta aac cag 645
 Trp Ala Leu Glu Leu Asn Gln
 210 215
 <210> 25
 <211> 411
 <212> PRT
 <213> Homo sapiens
 <400> 25
 Met Glu Arg Met Ser Asp Ser Ala Asp Lys Pro Ile Asp Asn Asp Ala
 1 5 10 15
 Glu Gly Val Trp Ser Pro Asp Ile Glu Gln Ser Phe Gln Glu Ala Leu
 20 25 30
 Ala Ile Tyr Pro Pro Cys Gly Arg Arg Lys Ile Ile Leu Ser Asp Glu
 35 40 45
 Gly Lys Met Tyr Gly Arg Asn Glu Leu Ile Ala Arg Tyr Ile Lys Leu
 50 55 60
 Arg Thr Gly Lys Thr Arg Thr Arg Lys Gln Val Ser Ser His Ile Gln
 65 70 75 80
 Val Leu Ala Arg Arg Lys Ser Arg Asp Phe His Ser Lys Leu Lys Asp
 85 90 95
 Gln Thr Ala Lys Asp Lys Ala Leu Gln His Met Ala Ala Met Ser Ser
 100 105 110
 Ala Gln Ile Val Ser Ala Thr Ala Ile His Asn Lys Leu Gly Leu Pro
 115 120 125
 Gly Ile Pro Arg Pro Thr Phe Pro Gly Ala Pro Gly Phe Trp Pro Gly
 130 135 140
 Met Ile Gln Thr Gly Gln Pro Gly Ser Ser Gln Asp Val Lys Pro Phe
 145 150 155 160
 Val Gln Gln Ala Tyr Pro Ile Gln Pro Ala Val Thr Ala Pro Ile Pro
 165 170 175
 Gly Phe Glu Pro Ala Ser Ala Pro Ala Pro Ser Val Pro Ala Trp Gln
 180 185 190
 Gly Arg Ser Ile Gly Thr Thr Lys Leu Arg Leu Val Glu Phe Ser Ala
 195 200 205
 Phe Leu Glu Gln Gln Arg Asp Pro Asp Ser Tyr Asn Lys His Leu Phe
 210 215 220
 Val His Ile Gly His Ala Asn His Ser Tyr Ser Asp Pro Leu Leu Glu
 225 230 235 240

Ser Val Asp Ile Arg Gln Ile Tyr Asp Lys Phe Pro Glu Lys Lys Gly
 245 250 255
 Gly Leu Lys Glu Leu Phe Gly Lys Gly Pro Gln Asn Ala Phe Phe Leu
 260 265 270
 Val Lys Phe Trp Ala Asp Leu Asn Cys Asn Ile Gln Asp Asp Ala Gly
 275 280 285
 Ala Phe Tyr Gly Val Thr Ser Gln Tyr Glu Ser Ser Glu Asn Met Thr
 290 295 300
 Val Thr Cys Ser Thr Lys Val Cys Ser Phe Gly Lys Gln Val Val Glu
 305 310 315 320
 Lys Val Glu Thr Glu Tyr Ala Arg Phe Glu Asn Gly Arg Phe Val Tyr
 325 330 335
 Arg Ile Asn Arg Ser Pro Met Cys Glu Tyr Met Ile Asn Phe Ile His
 340 345 350
 Lys Leu Lys His Leu Pro Glu Lys Tyr Met Met Asn Ser Val Leu Glu
 355 360 365
 Asn Phe Thr Ile Leu Leu Val Val Thr Asn Arg Asp Thr Gln Glu Thr
 370 375 380
 Leu Leu Cys Met Ala Cys Val Phe Glu Val Ser Asn Ser Glu His Gly
 385 390 395 400
 Ala Gln His His Ile Tyr Arg Leu Val Lys Asp
 405 410

<210> 26

<211> 1233

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1236)

<400> 26

atg gaa agg atg agt gac tct gca gat aag cca att gac aat gat gca 48
 Met Glu Arg Met Ser Asp Ser Ala Asp Lys Pro Ile Asp Asn Asp Ala
 1 5 10 15
 gaa ggg gtc tgg agc ccc gac atc gag caa agc ttt cag gag gcc ctg 96
 Glu Gly Val Trp Ser Pro Asp Ile Glu Gln Ser Phe Gln Glu Ala Leu
 20 25 30
 gct atc tat cca cca tgt ggg agg agg aaa atc atc tta tca gac gaa 144
 Ala Ile Tyr Pro Pro Cys Gly Arg Arg Lys Ile Ile Leu Ser Asp Glu
 35 40 45
 ggc aaa atg tat ggt agg aat gaa ttg ata gcc aga tac atc aaa ctc 192
 Gly Lys Met Tyr Gly Arg Asn Glu Leu Ile Ala Arg Tyr Ile Lys Leu
 50 55 60
 agg aca ggc aag acg agg acc aga aaa cag gtg tct agt cac att cag 240
 Arg Thr Gly Lys Thr Arg Thr Arg Lys Gln Val Ser Ser His Ile Gln
 65 70 75 80
 gtt ctt gcc aga agg aaa tct cgt gat ttt cat tcc aag cta aag gat 288

Val Leu Ala Arg Arg Lys Ser Arg Asp Phe His Ser Lys Leu Lys Asp
85 90 95
cag act gca aag gat aag gcc ctg cag cac atg gcg gcc atg tcc tca 336
Gln Thr Ala Lys Asp Lys Ala Leu Gln His Met Ala Ala Met Ser Ser
100 105 110
gcc cag atc gtc tgc gcc act gcc att cat aac aag ctg ggg ctg cct 384
Ala Gln Ile Val Ser Ala Thr Ala Ile His Asn Lys Leu Gly Leu Pro
115 120 125
ggg att cca cgc ccg acc ttc cca ggg gcg ccg ggg ttc tgg ccg gga 432
Gly Ile Pro Arg Pro Thr Phe Pro Gly Ala Pro Gly Phe Trp Pro Gly
130 135 140
atg att caa aca ggg cag cca gga tcc tca caa gac gtc aag cct ttt 480
Met Ile Gln Thr Gly Gln Pro Gly Ser Ser Gln Asp Val Lys Pro Phe
145 150 155 160
gtg cag cag gcc tac ccc atc cag cca gcg gtc aca gcc ccc att cca 528
Val Gln Gln Ala Tyr Pro Ile Gln Pro Ala Val Thr Ala Pro Ile Pro
165 170 175
ggg ttt gag cct gca tgc gcc cca gct ccc tca gtc cct gcc tgg caa 576
Gly Phe Glu Pro Ala Ser Ala Pro Ala Pro Ser Val Pro Ala Trp Gln
180 185 190
ggt cgc tcc att ggc aca acc aag ctt cgc ctg gtg gaa ttt tca gct 624
Gly Arg Ser Ile Gly Thr Thr Lys Leu Arg Leu Val Glu Phe Ser Ala
195 200 205
ttt ctc gag cag cag cga gac cca gac tgc tac aac aaa cac ctc ttc 672
Phe Leu Glu Gln Gln Arg Asp Pro Asp Ser Tyr Asn Lys His Leu Phe
210 215 220
gtg cac att ggg cat gcc aac cat tct tac agt gac cca ttg ctt gaa 720
Val His Ile Gly His Ala Asn His Ser Tyr Ser Asp Pro Leu Leu Glu
225 230 235 240
tca gtg gac att cgt cag att tat gac aaa ttt cct gaa aag aaa ggt 768
Ser Val Asp Ile Arg Gln Ile Tyr Asp Lys Phe Pro Glu Lys Lys Gly
245 250 255
ggc tta aag gaa ctg ttt gga aag ggc cct caa aat gcc ttc ttc ctc 816
Gly Leu Lys Glu Leu Phe Gly Lys Gly Pro Gln Asn Ala Phe Phe Leu
260 265 270
gta aaa ttc tgg gct gat tta aac tgc aat att caa gat gat gct ggg 864
Val Lys Phe Trp Ala Asp Leu Asn Cys Asn Ile Gln Asp Asp Ala Gly
275 280 285
gct ttt tat ggt gta acc agt cag tac gag agt tct gaa aat atg aca 912
Ala Phe Tyr Gly Val Thr Ser Gln Tyr Glu Ser Ser Glu Asn Met Thr
290 295 300
gtc acc tgt tcc acc aaa gtt tgc tcc ttt ggg aag caa gta gta gaa 960
Val Thr Cys Ser Thr Lys Val Cys Ser Phe Gly Lys Gln Val Val Glu
305 310 315 320
aaa gta gag acg gag tat gca agg ttt gag aat ggc cga ttt gta tac 1008
Lys Val Glu Thr Glu Tyr Ala Arg Phe Glu Asn Gly Arg Phe Val Tyr

325 330 335
 cga ata aac cgc tcc cca atg tgt gaa tat atg atc aac ttc atc cac 1056
 Arg Ile Asn Arg Ser Pro Met Cys Glu Tyr Met Ile Asn Phe Ile His
 340 345 350
 aag ctc aaa cac tta cca gag aaa tat atg atg aac agt gtt ttg gaa 1104
 Lys Leu Lys His Leu Pro Glu Lys Tyr Met Met Asn Ser Val Leu Glu
 355 360 365
 aac ttc aca att tta ttg gtg gta aca aac agg gat aca caa gaa act 1152
 Asn Phe Thr Ile Leu Leu Val Val Thr Asn Arg Asp Thr Gln Glu Thr
 370 375 380
 cta ctc tgc atg gcc tgt gtg ttt gaa gtt tca aat agt gaa cac gga 1200
 Leu Leu Cys Met Ala Cys Val Phe Glu Val Ser Asn Ser Glu His Gly
 385 390 395 400
 gca caa cat cat att tac agg ctt gta aag gac 1233
 Ala Gln His His Ile Tyr Arg Leu Val Lys Asp
 405 410
 <210> 27
 <211> 427
 <212> PRT
 <213> Homo sapiens
 <400> 27
 Ile Thr Ser Asn Glu Trp Ser Ser Pro Thr Ser Pro Glu Gly Ser Thr
 1 5 10 15
 Ala Ser Gly Gly Ser Gln Ala Leu Asp Lys Pro Ile Asp Asn Asp Ala
 20 25 30
 Glu Gly Val Trp Ser Pro Asp Ile Glu Gln Ser Phe Gln Glu Ala Leu
 35 40 45
 Ala Ile Tyr Pro Pro Cys Gly Arg Arg Lys Ile Ile Leu Ser Asp Glu
 50 55 60
 Gly Lys Met Tyr Gly Arg Asn Glu Leu Ile Ala Arg Tyr Ile Lys Leu
 65 70 75 80
 Arg Thr Gly Lys Thr Arg Thr Arg Lys Gln Val Ser Ser His Ile Gln
 85 90 95
 Val Leu Ala Arg Arg Lys Ala Arg Glu Ile Gln Ala Lys Leu Lys Asp
 100 105 110
 Gln Ala Ala Lys Asp Lys Ala Leu Gln Ser Met Ala Ala Met Ser Ser
 115 120 125
 Ala Gln Ile Ile Ser Ala Thr Ala Phe His Ser Ser Met Ala Leu Ala
 130 135 140
 Arg Gly Pro Gly Arg Pro Ala Val Ser Gly Phe Trp Gln Gly Ala Leu
 145 150 155 160
 Pro Gly Gln Ala Gly Thr Ser His Asp Val Lys Pro Phe Ser Gln Gln
 165 170 175
 Thr Tyr Ala Val Gln Pro Pro Leu Pro Leu Pro Gly Phe Glu Ser Pro
 180 185 190
 Ala Gly Pro Ala Pro Ser Pro Ser Ala Pro Pro Ala Pro Pro Trp Gln

195	200	205	
Gly Arg Ser Val Ala Ser Ser Lys Leu Trp Met Leu Glu Phe Ser Ala			
210	215	220	
Phe Leu Glu Gln Gln Gln Asp Pro Asp Thr Tyr Asn Lys His Leu Phe			
225	230	235	240
Val His Ile Gly Gln Ser Ser Pro Ser Tyr Ser Asp Pro Tyr Leu Glu			
245	250	255	
Ala Val Asp Ile Arg Gln Ile Tyr Asp Lys Phe Pro Glu Lys Lys Gly			
260	265	270	
Gly Leu Lys Asp Leu Phe Glu Arg Gly Pro Ser Asn Ala Phe Phe Leu			
275	280	285	
Val Lys Phe Trp Ala Asp Leu Asn Thr Asn Ile Glu Asp Glu Gly Ser			
290	295	300	
Ser Phe Tyr Gly Val Ser Ser Gln Tyr Glu Ser Pro Glu Asn Met Ile			
305	310	315	320
Ile Thr Cys Ser Thr Lys Val Cys Ser Phe Gly Lys Gln Val Val Glu			
325	330	335	
Lys Val Glu Thr Glu Tyr Ala Arg Tyr Glu Asn Gly His Tyr Ser Tyr			
340	345	350	
Arg Ile His Arg Ser Pro Leu Cys Glu Tyr Met Ile Asn Phe Ile His			
355	360	365	
Lys Leu Lys His Leu Pro Glu Lys Tyr Met Met Asn Ser Val Leu Glu			
370	375	380	
Asn Phe Thr Ile Leu Gln Val Val Thr Asn Arg Asp Thr Gln Glu Thr			
385	390	395	400
Leu Leu Cys Ile Ala Tyr Val Phe Glu Val Ser Ala Ser Glu His Gly			
405	410	415	
Ala Gln His His Ile Tyr Arg Leu Val Lys Glu			
420	425		

<210> 28

<211> 1281

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1284)

<400> 28

att acc tcc aac gag tgg agc tct ccc acc tcc cct gag ggg agc acc 48

Ile Thr Ser Asn Glu Trp Ser Ser Pro Thr Ser Pro Glu Gly Ser Thr

1 5 10 15

gcc tct ggg ggc agt cag gca ctg gac aag ccc atc gac aat gac gca 96

Ala Ser Gly Gly Ser Gln Ala Leu Asp Lys Pro Ile Asp Asn Asp Ala

20 25 30

gag ggc gtg tgg agc ccg gat att gag cag agt ttc cag gag gcc ctc 144

Glu Gly Val Trp Ser Pro Asp Ile Glu Gln Ser Phe Gln Glu Ala Leu

35 40 45

gcc atc tac ccg ccc tgt ggc agg cgc aaa atc atc ctg tgc gac gag 192
 Ala Ile Tyr Pro Pro Cys Gly Arg Arg Lys Ile Ile Leu Ser Asp Glu
 50 55 60
 ggc aag atg tat ggt cgg aac gag ctg att gcc cgc tac atc aag ctc 240
 Gly Lys Met Tyr Gly Arg Asn Glu Leu Ile Ala Arg Tyr Ile Lys Leu
 65 70 75 80
 cgg aca ggg aag acc cgc acc agg aag cag gtc tcc agc cac atc cag 288
 Arg Thr Gly Lys Thr Arg Thr Arg Lys Gln Val Ser Ser His Ile Gln
 85 90 95
 gtg ctg gct cgt cgc aaa gct cgc gag atc cag gcc aag cta aag gac 336
 Val Leu Ala Arg Arg Lys Ala Arg Glu Ile Gln Ala Lys Leu Lys Asp
 100 105 110
 cag gca gct aag gac aag gcc ctg cag agc atg gct gcc atg tgc tct 384
 Gln Ala Ala Lys Asp Lys Ala Leu Gln Ser Met Ala Ala Met Ser Ser
 115 120 125
 gca cag atc atc tcc gcc acg gcc ttc cac agt agc atg gcc ctc gcc 432
 Ala Gln Ile Ile Ser Ala Thr Ala Phe His Ser Ser Met Ala Leu Ala
 130 135 140
 cgg ggc ccc ggc cgc cca gca gtc tca ggg ttt tgg caa gga gct ttg 480
 Arg Gly Pro Gly Arg Pro Ala Val Ser Gly Phe Trp Gln Gly Ala Leu
 145 150 155 160
 cca ggc caa gcc gga acg tcc cat gat gtg aag cct ttc tct cag caa 528
 Pro Gly Gln Ala Gly Thr Ser His Asp Val Lys Pro Phe Ser Gln Gln
 165 170 175
 acc tat gct gtc cag cct ccg ctg cct ctg cca ggg ttt gag tct cct 576
 Thr Tyr Ala Val Gln Pro Pro Leu Pro Pro Gly Phe Glu Ser Pro
 180 185 190
 gca ggg ccc gcc cca tgc ccc tct gcg ccc ccg gca ccc cca tgg cag 624
 Ala Gly Pro Ala Pro Ser Pro Ser Ala Pro Pro Ala Pro Pro Trp Gln
 195 200 205
 ggc cgc agc gtg gcc agc tcc aag ctc tgg atg ttg gag ttc tct gcc 672
 Gly Arg Ser Val Ala Ser Ser Lys Leu Trp Met Leu Glu Phe Ser Ala
 210 215 220
 ttc ctg gag cag cag cag gac ccg gac acg tac aac aag cac ctg ttc 720
 Phe Leu Glu Gln Gln Gln Asp Pro Asp Thr Tyr Asn Lys His Leu Phe
 225 230 235 240
 gtg cac att ggc cag tcc agc cca agc tac agc gac ccc tac ctc gaa 768
 Val His Ile Gly Gln Ser Ser Pro Ser Tyr Ser Asp Pro Tyr Leu Glu
 245 250 255
 gcc gtg gac atc cgc caa atc tat gac aaa ttc ccg gag aaa aag ggt 816
 Ala Val Asp Ile Arg Gln Ile Tyr Asp Lys Phe Pro Glu Lys Lys Gly
 260 265 270
 gga ctc aag gat ctc ttc gaa cgg gga ccc tcc aat gcc ttt ttt ctt 864
 Gly Leu Lys Asp Leu Phe Glu Arg Gly Pro Ser Asn Ala Phe Phe Leu
 275 280 285
 gtg aag ttc tgg gca gac ctc aac acc aac atc gag gat gaa ggc agc 912

Val Lys Phe Trp Ala Asp Leu Asn Thr Asn Ile Glu Asp Glu Gly Ser
290 295 300
tcc ttc tat ggg gtc tcc agc cag tat gag agc ccc gag aac atg atc 960
Ser Phe Tyr Gly Val Ser Ser Gln Tyr Glu Ser Pro Glu Asn Met Ile
305 310 315 320
atc acc tgc tcc acg aag gtc tgc tct ttc ggc aag cag gtg gtg gag 1008
Ile Thr Cys Ser Thr Lys Val Cys Ser Phe Gly Lys Gln Val Val Glu
325 330 335
aaa gtt gag aca gag tat gct cgc tat gag aat gga cac tac tct tac 1056
Lys Val Glu Thr Glu Tyr Ala Arg Tyr Glu Asn Gly His Tyr Ser Tyr
340 345 350
cgc atc cac cgg tcc ccg ctc tgt gag tac atg atc aac ttc atc cac 1104
Arg Ile His Arg Ser Pro Leu Cys Glu Tyr Met Ile Asn Phe Ile His
355 360 365
aag ctc aag cac ctc cct gag aag tac atg atg aac agc gtg ctg gag 1152
Lys Leu Lys His Leu Pro Glu Lys Tyr Met Met Asn Ser Val Leu Glu
370 375 380
aac ttc acc atc ctg cag gtg gtc acc aac aga gac aca cag gag acc 1200
Asn Phe Thr Ile Leu Gln Val Val Thr Asn Arg Asp Thr Gln Glu Thr
385 390 395 400
ttg ctg tgc att gcc tat gtc ttt gag gtg tca gcc agt gag cac ggg 1248
Leu Leu Cys Ile Ala Tyr Val Phe Glu Val Ser Ala Ser Glu His Gly
405 410 415
gct cag cac cac atc tac agg ctg gtg aaa gaa 1281
Ala Gln His His Ile Tyr Arg Leu Val Lys Glu
420 425
<210> 29
<211> 435
<212> PRT
<213> Homo sapiens
<400> 29
Ile Ala Ser Asn Ser Trp Asn Ala Ser Ser Ser Pro Gly Glu Ala Arg
1 5 10 15
Glu Asp Gly Pro Glu Gly Leu Asp Lys Gly Leu Asp Asn Asp Ala Glu
20 25 30
Gly Val Trp Ser Pro Asp Ile Glu Gln Ser Phe Gln Glu Ala Leu Ala
35 40 45
Ile Tyr Pro Pro Cys Gly Arg Arg Lys Ile Ile Leu Ser Asp Glu Gly
50 55 60
Lys Met Tyr Gly Arg Asn Glu Leu Ile Ala Arg Tyr Ile Lys Leu Arg
65 70 75 80
Thr Gly Lys Thr Arg Thr Arg Lys Gln Val Ser Ser His Ile Gln Val
85 90 95
Leu Ala Arg Lys Lys Val Arg Glu Tyr Gln Val Gly Ile Lys Ala Met
100 105 110
Asn Leu Asp Gln Val Ser Lys Asp Lys Ala Leu Gln Ser Met Ala Ser

115	120	125	
Met Ser Ser Ala Gln Ile Val Ser Ala Ser Val Leu Gln Asn Lys Phe			
130	135	140	
Ser Pro Pro Ser Pro Leu Pro Gln Ala Val Phe Ser Thr Ser Ser Arg			
145	150	155	160
Phe Trp Ser Ser Pro Pro Leu Leu Gly Gln Gln Pro Gly Pro Ser Gln			
165	170	175	
Asp Ile Lys Pro Phe Ala Gln Pro Ala Tyr Pro Ile Gln Pro Pro Leu			
180	185	190	
Pro Pro Thr Leu Ser Ser Tyr Glu Pro Leu Ala Pro Leu Pro Ser Ala			
195	200	205	
Ala Ala Ser Val Pro Val Trp Gln Asp Arg Thr Ile Ala Ser Ser Arg			
210	215	220	
Leu Arg Leu Leu Glu Tyr Ser Ala Phe Met Glu Val Gln Arg Asp Pro			
225	230	235	240
Asp Thr Tyr Ser Lys His Leu Phe Val His Ile Gly Gln Thr Asn Pro			
245	250	255	
Ala Phe Ser Asp Pro Pro Leu Glu Ala Val Asp Val Arg Gln Ile Tyr			
260	265	270	
Asp Lys Phe Pro Glu Lys Lys Gly Gly Leu Lys Glu Leu Tyr Glu Lys			
275	280	285	
Gly Pro Pro Asn Ala Phe Phe Leu Val Lys Phe Trp Ala Asp Leu Asn			
290	295	300	
Ser Thr Ile Gln Glu Gly Pro Gly Ala Phe Tyr Gly Val Ser Ser Gln			
305	310	315	320
Tyr Ser Ser Ala Asp Ser Met Thr Ile Ser Val Ser Thr Lys Val Cys			
325	330	335	
Ser Phe Gly Lys Gln Val Val Glu Lys Val Glu Thr Glu Tyr Ala Arg			
340	345	350	
Leu Glu Asn Gly Arg Phe Val Tyr Arg Ile His Arg Ser Pro Met Cys			
355	360	365	
Glu Tyr Met Ile Asn Phe Ile His Lys Lys Leu Lys His Leu Pro Glu Lys			
370	375	380	
Tyr Met Met Asn Ser Val Leu Glu Asn Phe Thr Ile Leu Gln Val Val			
385	390	395	400
Thr Ser Arg Asp Ser Gln Glu Thr Leu Leu Val Ile Ala Phe Val Phe			
405	410	415	
Glu Val Ser Thr Ser Glu His Gly Ala Gln His His Val Tyr Lys Leu			
420	425	430	
Val Lys Asp			

<210> 30

<211> 1305

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1305)

<400> 30

ata gcg tcc aac agc tgg aac gcc agc agc agc ccc ggg gag gcc cgg 48
Ile Ala Ser Asn Ser Trp Asn Ala Ser Ser Ser Pro Gly Glu Ala Arg

1 5 10 15

gag gat ggg ccc gag ggc ctg gac aag ggg ctg gac aac gat gcg gag 96
Glu Asp Gly Pro Glu Gly Leu Asp Lys Gly Leu Asp Asn Asp Ala Glu
20 25 30

ggc gtg tgg agc ccg gac atc gag cag agc ttc cag gag gcc ctg gcc 144
Gly Val Trp Ser Pro Asp Ile Glu Gln Ser Phe Gln Glu Ala Leu Ala
35 40 45

atc tac ccg ccc tgc ggc cgg cgg aag atc atc ctg tca gac gag ggc 192
Ile Tyr Pro Pro Cys Gly Arg Arg Lys Ile Ile Leu Ser Asp Glu Gly
50 55 60

aag atg tac ggc cga aat gag ttg att gca cgc tat att aaa ctg agg 240
Lys Met Tyr Gly Arg Asn Glu Leu Ile Ala Arg Tyr Ile Lys Leu Arg
65 70 75 80

acg ggg aag act cgg acg aga aaa cag gtg tcc agc cac ata cag gtt 288
Thr Gly Lys Thr Arg Thr Arg Lys Gln Val Ser Ser His Ile Gln Val
85 90 95

cta gct cgg aag aag gtg cgg gag tac cag gtt ggc atc aag gcc atg 336
Leu Ala Arg Lys Lys Val Arg Glu Tyr Gln Val Gly Ile Lys Ala Met
100 105 110

aac ctg gac cag gtc tcc aag gac aaa gcc ctt cag agc atg gcg tcc 384
Asn Leu Asp Gln Val Ser Lys Asp Lys Ala Leu Gln Ser Met Ala Ser
115 120 125

atg tcc tct gcc cag atc gtc tct gcc agt gtc ctg cag aac aag ttc 432
Met Ser Ser Ala Gln Ile Val Ser Ala Ser Val Leu Gln Asn Lys Phe
130 135 140

agc cca cct tcc cct ctg ccc cag gcc gtc ttc tcc act tcc tcg cgg 480
Ser Pro Pro Ser Pro Leu Pro Gln Ala Val Phe Ser Thr Ser Ser Arg
145 150 155 160

ttc tgg agc agc ccc cct ctc ctg gga cag cag cct gga ccc tct cag 528
Phe Trp Ser Ser Pro Pro Leu Leu Gly Gln Gln Pro Gly Pro Ser Gln
165 170 175

gac atc aag ccc ttt gca cag cca gcc tac ccc atc cag ccg ccc ctg 576
Asp Ile Lys Pro Phe Ala Gln Pro Ala Tyr Pro Ile Gln Pro Pro Leu
180 185 190

ccg ccg acg ctc agc agt tat gag ccc ctg gcc ccg ctc ccc tca gct 624
Pro Pro Thr Leu Ser Ser Tyr Glu Pro Leu Ala Pro Leu Pro Ser Ala
195 200 205

gct gcc tct gtg cct gtg tgg cag gac cgt acc att gcc tcc tcc cgg 672
Ala Ala Ser Val Pro Val Trp Gln Asp Arg Thr Ile Ala Ser Ser Arg
210 215 220

ctg cgg ctc ctg gag tat tca gcc ttc atg gag gtg cag cga gac cct 720
Leu Arg Leu Leu Glu Tyr Ser Ala Phe Met Glu Val Gln Arg Asp Pro

225 230 235 240
gac acg tac agc aaa cac ctg ttt gtg cac atc ggc cag acg aac ccc 768
Asp Thr Tyr Ser Lys His Leu Phe Val His Ile Gly Gln Thr Asn Pro
245 250 255
gcc ttc tca gac cca ccc ctg gag gca gta gat gtg cgc cag atc tat 816
Ala Phe Ser Asp Pro Pro Leu Glu Ala Val Asp Val Arg Gln Ile Tyr
260 265 270
gac aaa ttc ccc gag aaa aag gga gga ttg aag gag ctc tat gag aag 864
Asp Lys Phe Pro Glu Lys Lys Gly Gly Leu Lys Glu Leu Tyr Glu Lys
275 280 285
ggg ccc cct aat gcc ttc ttc ctt gtc aag ttc tgg gcc gac ctc aac 912
Gly Pro Pro Asn Ala Phe Phe Leu Val Lys Phe Trp Ala Asp Leu Asn
290 295 300
agc acc atc cag gag ggc cgg gga gcc ttc tat ggg gtc agc tct cag 960
Ser Thr Ile Gln Glu Gly Pro Gly Ala Phe Tyr Gly Val Ser Ser Gln
305 310 315 320
tac agc tct gct gat agc atg acc atc agc gtc tcc acc aag gtg tgc 1008
Tyr Ser Ser Ala Asp Ser Met Thr Ile Ser Val Ser Thr Lys Val Cys
325 330 335
tcc ttt ggc aaa cag gtg gta gag aag gtg gag act gag tat gcc agg 1056
Ser Phe Gly Lys Gln Val Val Glu Lys Val Glu Thr Glu Tyr Ala Arg
340 345 350
ctg gag aac ggg cgc ttt gtg tac cgt atc cac cgc tcg ccc atg tgc 1104
Leu Glu Asn Gly Arg Phe Val Tyr Arg Ile His Arg Ser Pro Met Cys
355 360 365
gag tac atg atc aac ttc atc cac aag ctg aag cac ctg ccc gag aag 1152
Glu Tyr Met Ile Asn Phe Ile His Lys Leu Lys His Leu Pro Glu Lys
370 375 380
tac atg atg aac agc gtg ctg gag aac ttc acc atc ctg cag gtg gtc 1200
Tyr Met Met Asn Ser Val Leu Glu Asn Phe Thr Ile Leu Gln Val Val
385 390 395 400
acg agc cgg gac tcc cag gag acc ttg ctt gtc att gct ttt gtc ttc 1248
Thr Ser Arg Asp Ser Gln Glu Thr Leu Leu Val Ile Ala Phe Val Phe
405 410 415
gaa gtc tcc acc agt gag cac ggg gcc cag cac cat gtc tac aag ctc 1296
Glu Val Ser Thr Ser Glu His Gly Ala Gln His His Val Tyr Lys Leu
420 425 430
gtc aaa gac
Val Lys Asp
435
<210> 31
<211> 1132
<212> PRT
<213> Homo sapiens
<400> 31
Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser

1 5 10 15
His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
20 25 30
Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
35 40 45
Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
50 55 60
Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
65 70 75 80
Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
85 90 95
Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
100 105 110
Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
115 120 125
Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
130 135 140
Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
145 150 155 160
Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
165 170 175
Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
180 185 190
Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
195 200 205
Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
210 215 220
Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
225 230 235 240
Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
245 250 255
Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
260 265 270
Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
275 280 285
Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
290 295 300
Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
305 310 315 320
Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
325 330 335
Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
340 345 350
Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
355 360 365
Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln

370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His

740	745	750	
Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp			
755	760	765	
Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser			
770	775	780	
Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu			
785	790	795	800
Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His			
805	810	815	
Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro			
820	825	830	
Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp			
835	840	845	
Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu			
850	855	860	
Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala			
865	870	875	880
Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys			
885	890	895	
Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu			
900	905	910	
Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe			
915	920	925	
Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser			
930	935	940	
Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe			
945	950	955	960
Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly			
965	970	975	
Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn			
980	985	990	
Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln			
995	1000	1005	
Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln			
1010	1015	1020	
Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala			
1025	1030	1035	1040
Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu			
1045	1050	1055	
Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp			
1060	1065	1070	
Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr			
1075	1080	1085	
Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser			
1090	1095	1100	
Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn			

1105 1110 1115 1120
Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1125 1130

<210> 32

<211> 3396

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(3399)

<400> 32

atg ccg cgc gct ccc cgc tgc cga gcc gtg cgc tcc ctg ctg cgc agc 48

Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser

1 5 10 15

cac tac cgc gag gtg ctg ccg ctg gcc acg ttc gtg cgg cgc ctg ggg 96

His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly

20 25 30

ccc cag gcc tgg cgg ctg gtg cag cgc ggg gac ccg gcg gct ttc cgc 144

Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg

35 40 45

gcg ctg gtg gcc cag tgc ctg gtg tgc gtg ccc tgg gac gca cgg ccg 192

Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro

50 55 60

ccc ccc gcc gcc ccc tcc ttc cgc cag gtg tcc tgc ctg aag gag ctg 240

Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu

65 70 75 80

gtg gcc cga gtg ctg cag agg ctg tgc gag cgc gcc gcg aag aac gtg 288

Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val

85 90 95

ctg gcc ttc gcc ttc gcg ctg ctg gac ggg gcc cgc ggg gcc ccc ccc 336

Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro

100 105 110

gag gcc ttc acc acc agc gtg cgc agc tac ctg ccc aac acg gtg acc 384

Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr

115 120 125

gac gca ctg cgg ggg agc ggg gcg tgg ggg ctg ctg ctg cgc cgc gtg 432

Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val

130 135 140

ggc gac gac gtg ctg gtt cac ctg ctg gca cgc tgc gcg ctc ttt gtg 480

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val

145 150 155 160

ctg gtg gct ccc agc tgc gcc tac cag gtg tgc ggg ccg ccg ctg tac 528

Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr

165 170 175

cag ctc gcc gct gcc act cag gcc cgg ccc ccg cca cac gct agt gga 576

Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly

180	185	190	
ccc cga agg cgt ctg gga tgc gaa cgg gcc tgg aac cat agc gtc agg	624		
Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg			
195	200	205	
gag gcc ggg gtc ccc ctg ggc ctg cca gcc ccg ggt gcg agg agg cgc	672		
Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg			
210	215	220	
ggg ggc agt gcc agc cga agt ctg ccg ttg ccc aag agg ccc agg cgt	720		
Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg			
225	230	235	240
ggc gct gcc cct gag ccg gag cgg acg ccc gtt ggg cag ggg tcc tgg	768		
Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp			
245	250	255	
gcc cac ccg ggc agg acg cgt gga ccg agt gac cgt ggt ttc tgt gtg	816		
Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val			
260	265	270	
gtg tca cct gcc aga ccc gcc gaa gaa gcc acc tct ttg gag ggt gcg	864		
Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala			
275	280	285	
ctc tct ggc acg cgc cac tcc cac cca tcc gtg ggc cgc cag cac cac	912		
Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His			
290	295	300	
gcg ggc ccc cca tcc aca tgc cgg cca cca cgt ccc tgg gac acg cct	960		
Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro			
305	310	315	320
tgt ccc ccg gtg tac gcc gag acc aag cac ttc ctc tac tcc tca ggc	1008		
Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly			
325	330	335	
gac aag gag cag ctg cgg ccc tcc ttc cta ctc agc tct ctg agg ccc	1056		
Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro			
340	345	350	
agc ctg act ggc gct cgg agg ctc gtg gag acc atc ttt ctg ggt tcc	1104		
Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser			
355	360	365	
agg ccc tgg atg cca ggg act ccc cgc agg ttg ccc cgc ctg ccc cag	1152		
Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln			
370	375	380	
cgc tac tgg caa atg cgg ccc ctg ttt ctg gag ctg ctt ggg aac cac	1200		
Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His			
385	390	395	400
gcg cag tgc ccc tac ggg gtg ctc ctc aag acg cac tgc ccg ctg cga	1248		
Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg			
405	410	415	
gct gcg gtc acc cca gca gcc ggt gtc tgt gcc cgg gag aag ccc cag	1296		
Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln			
420	425	430	

ggc tct gtg gcg gcc ccc gag gag gag gac aca gac ccc cgt cgc ctg 1344
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 gtg cag ctg ctc cgc cag cac agc agc ccc tgg cag gtg tac ggc ttc 1392
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 gtg cgg gcc tgc ctg cgc cgg ctg gtg ccc cca ggc ctc tgg ggc tcc 1440
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 agg cac aac gaa cgc cgc ttc ctc agg aac acc aag aag ttc atc tcc 1488
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 ctg ggg aag cat gcc aag ctc tcg ctg cag gag ctg acg tgg aag atg 1536
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510
 agc gtg cgg gac tgc gct tgg ctg cgc agg agc cca ggg gtt ggc tgt 1584
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 gtt ccg gcc gca gag cac cgt ctg cgt gag gag atc ctg gcc aag ttc 1632
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
 ctg cac tgg ctg atg agt gtg tac gtc gtc gag ctg ctc agg tct ttc 1680
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 ttt tat gtc acg gag acc acg ttt caa aag aac agg ctc ttt ttc tac 1728
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 cgg aag agt gtc tgg agc aag ttg caa agc att gga atc aga cag cac 1776
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590
 ttg aag agg gtg cag ctg cgg gag ctg tcg gaa gca gag gtc agg cag 1824
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 cat cgg gaa gcc agg ccc gcc ctg ctg acg tcc aga ctc cgc ttc atc 1872
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 ccc aag cct gac ggg ctg cgg ccg att gtg aac atg gac tac gtc gtg 1920
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 gga gcc aga acg ttc cgc aga gaa aag agg gcc gag cgt ctc acc tcg 1968
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 agg gtg aag gca ctg ttc agc gtg ctc aac tac gag cgg gcg cgg cgc 2016
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 ccc ggc ctc ctg ggc gcc tct gtg ctg ggc ctg gac gat atc cac agg 2064

Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 gcc tgg cgc acc ttc gtg ctg cgt gtg cgg gcc cag gac ccg ccg cct 2112
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 gag ctg tac ttt gtc aag gtg gat gtg acg ggc gcg tac gac acc atc 2160
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720
 ccc cag gac agg ctc acg gag gtc atc gcc agc atc atc aaa ccc cag 2208
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735
 aac acg tac tgc gtg cgt cgg tat gcc gtg gtc cag aag gcc gcc cat 2256
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750
 ggg cac gtc cgc aag gcc ttc aag agc cac gtc tct acc ttg aca gac 2304
 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
 755 760 765
 ctc cag ccg tac atg cga cag ttc gtg gct cac ctg cag gag acc agc 2352
 Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
 770 775 780
 ccg ctg agg gat gcc gtc gtc atc gag cag agc tcc tcc ctg aat gag 2400
 Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
 785 790 795 800
 gcc agc agt ggc ctc ttc gac gtc ttc cta cgc ttc atg tgc cac cac 2448
 Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
 805 810 815
 gcc gtg cgc atc agg ggc aag tcc tac gtc cag tgc cag ggg atc ccg 2496
 Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
 820 825 830
 cag ggc tcc atc ctc tcc acg ctg ctc tgc agc ctg tgc tac ggc gac 2544
 Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
 835 840 845
 atg gag aac aag ctg ttt gcg ggg att cgg cgg gac ggg ctg ctc ctg 2592
 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
 850 855 860
 cgt ttg gtg gat gat ttc ttg ttg gtg aca cct cac ctc acc cac gcg 2640
 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
 865 870 875 880
 aaa acc ttc ctc agg acc ctg gtc cga ggt gtc cct gag tat ggc tgc 2688
 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
 885 890 895
 gtg gtg aac ttg cgg aag aca gtg gtg aac ttc cct gta gaa gac gag 2736
 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
 900 905 910
 gcc ctg ggt ggc acg gct ttt gtt cag atg ccg gcc cac ggc cta ttc 2784
 Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe

915 920 925
 ccc tgg tgc ggc ctg ctg ctg gat acc cgg acc ctg gag gtg cag agc 2832
 Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
 930 935 940
 gac tac tcc agc tat gcc cgg acc tcc atc aga gcc agt ctc acc ttc 2880
 Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
 945 950 955 960
 aac cgc ggc ttc aag gct ggg agg aac atg cgt cgc aaa ctc ttt ggg 2928
 Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
 965 970 975
 gtc ttg cgg ctg aag tgt cac agc ctg ttt ctg gat ttg cag gtg aac 2976
 Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
 980 985 990
 agc ctc cag acg gtg tgc acc aac atc tac aag atc ctc ctg ctg cag 3024
 Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln
 995 1000 1005
 gcg tac agg ttt cac gca tgt gtg ctg cag ctc cca ttt cat cag caa 3072
 Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
 1010 1015 1020
 gtt tgg aag aac ccc aca ttt ttc ctg cgc gtc atc tct gac acg gcc 3120
 Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
 1025 1030 1035 1040
 tcc ctc tgc tac tcc atc ctg aaa gcc aag aac gca ggg atg tgc ctg 3168
 Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
 1045 1050 1055
 ggg gcc aag ggc gcc gcc ggc cct ctg ccc tcc gag gcc gtg cag tgg 3216
 Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
 1060 1065 1070
 ctg tgc cac caa gca ttc ctg ctc aag ctg act cga cac cgt gtc acc 3264
 Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
 1075 1080 1085
 tac gtg cca ctc ctg ggg tca ctc agg aca gcc cag acg cag ctg agt 3312
 Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
 1090 1095 1100
 cgg aag ctc ccg ggg acg acg ctg act gcc ctg gag gcc gca gcc aac 3360
 Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn
 1105 1110 1115 1120
 ccg gca ctg ccc tca gac ttc aag acc atc ctg gac 3396
 Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1125 1130

<210> 33

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 33
 ttggcttcca ggccataatt g 21
 <210> 34
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: artificially synthesized primer sequence
 <400> 34
 aagagggcag atctatcgga 20
 <210> 35
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: artificially synthesized primer sequence
 <400> 35
 atggatctcc tgaagtgct 20
 <210> 36
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: artificially synthesized primer sequence
 <400> 36
 aagagggcag atctatcgga 20
 <210> 37
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: artificially synthesized primer sequence
 <400> 37
 ggaagagtga gcggccatca agg 23
 <210> 38
 <211> 22
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: artificially synthesized primer sequence
 <400> 38
 ctgctggaga gggtattcct cg 22
 <210> 39
 <211> 24
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 39

gccaaacacca acctgtccaa gttc

24

<210> 40

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 40

tgcaaaggct ccaggtctga gggc

24

<210> 41

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 41

ctctctctcc tcaggacaa

19

<210> 42

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 42

tggagcaaaa cagaatggct gg

22

<210> 43

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 43

ctgagatgtc tctctcttc ttag

24

<210> 44

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 44

acaatgactg atgagagatg

20

<210> 45

<211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: artificially synthesized primer sequence
 <400> 45
 cagacctgaa ggagacct 18
 <210> 46
 <211> 18
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: artificially synthesized primer sequence
 <400> 46
 gtcagcgtaa acagttgc 18
 <210> 47
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: artificially synthesized primer sequence
 <400> 47
 gccaaagaagc ggatagaagg 20
 <210> 48
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: artificially synthesized primer sequence
 <400> 48
 ctgtggttca gggctcagtc 20
 <210> 49
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: artificially synthesized primer sequence
 <400> 49
 cagtggagct ggacaaagcc 20
 <210> 50
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: artificially synthesized primer sequence
 <400> 50

tagcgacggt tctggaacca	20
<210> 51	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: artificially synthesized primer sequence	
<400> 51	
ctgtcatctc actatgggca	20
<210> 52	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: artificially synthesized primer sequence	
<400> 52	
ccaagtccga gcaggaattt	20
<210> 53	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: artificially synthesized primer sequence	
<400> 53	
aagacgtcaa gccctttgtg	20
<210> 54	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: artificially synthesized primer sequence	
<400> 54	
aaaggagcac actttggtgg	20
<210> 55	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence: artificially synthesized primer sequence	
<400> 55	
agcaagaata cgatgccatc	20
<210> 56	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	

<223>Description of Artificial Sequence: artificially synthesized primer sequence

<400> 56

gaaggggtgg tggtaggctc 20

<210> 57

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 57

tgggaatggc tatgtcagtg 20

<210> 58

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 58

ctggtaatct gtgtgtagg 20

<210> 59

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 59

caagggcctc tccaaacttg 20

<210> 60

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 60

gccccagaga cagcattcca 20

<210> 61

<211> 268

<212> PRT

<213> Homo sapiens

<400> 61

Met Ala Gln Pro Leu Cys Pro Pro Leu Ser Glu Ser Trp Met Leu Ser

1 5 10 15

Ala Ala Trp Gly Pro Thr Arg Arg Pro Pro Pro Ser Asp Lys Asp Cys

20 25 30

Gly Arg Ser Leu Val Ser Ser Pro Asp Ser Trp Gly Ser Thr Pro Ala
35 40 45

Asp Ser Pro Val Ala Ser Pro Ala Arg Pro Gly Thr Leu Arg Asp Pro
50 55 60

Arg Ala Pro Ser Val Gly Arg Arg Gly Ala Arg Ser Ser Arg Leu Gly
65 70 75 80

Ser Gly Gln Arg Gln Ser Ala Ser Glu Arg Glu Lys Leu Arg Met Arg
85 90 95

Thr Leu Ala Arg Ala Leu His Glu Leu Arg Arg Phe Leu Pro Pro Ser
100 105 110

Val Ala Pro Ala Gly Gln Ser Leu Thr Lys Ile Glu Thr Leu Arg Leu
115 120 125

Ala Ile Arg Tyr Ile Gly His Leu Ser Ala Val Leu Gly Leu Ser Glu
130 135 140

Glu Ser Leu Gln Arg Arg Cys Arg Gln Arg Gly Asp Ala Gly Ser Pro
145 150 155 160

Arg Gly Cys Pro Leu Cys Pro Asp Asp Cys Pro Ala Gln Met Gln Thr
165 170 175

Arg Thr Gln Ala Glu Gly Gln Gly Gln Gly Arg Gly Leu Gly Leu Val
180 185 190

Ser Ala Val Arg Ala Gly Ala Ser Trp Gly Ser Pro Pro Ala Cys Pro
195 200 205

Gly Ala Arg Ala Ala Pro Glu Pro Arg Asp Pro Pro Ala Leu Phe Ala
210 215 220

Glu Ala Ala Cys Pro Glu Gly Gln Ala Met Glu Pro Ser Pro Pro Ser
225 230 235 240

Pro Leu Leu Pro Gly Asp Val Leu Ala Leu Leu Glu Thr Trp Met Pro
245 250 255

Leu Ser Pro Leu Glu Trp Leu Pro Glu Glu Pro Lys
260 265

<210> 62

<211> 804

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(807)

<400> 62

atg gcc cag ccc ctg tgc ccg ccg ctc tcc gag tcc tgg atg ctc tct 48
Met Ala Gln Pro Leu Cys Pro Pro Leu Ser Glu Ser Trp Met Leu Ser
1 5 10 15

gcg gcc tgg ggc cca act cgg cgg ccg ccc tcc gac aag gac tgc 96
Ala Ala Trp Gly Pro Thr Arg Arg Pro Pro Pro Ser Asp Lys Asp Cys
20 25 30

ggc cgc tcc ctc gtc tgc tcc cca gac tca tgg ggc agc acc cca gcc 144
Gly Arg Ser Leu Val Ser Ser Pro Asp Ser Trp Gly Ser Thr Pro Ala
35 40 45

gac agc ccc gtg gcg agc ccc gcg cgg cca ggc acc ctc cgg gac ccc 192
Asp Ser Pro Val Ala Ser Pro Ala Arg Pro Gly Thr Leu Arg Asp Pro
50 55 60

cgc gcc ccc tcc gta ggt agg cgc ggc gcg cgc agc agc cgc ctg ggc 240
Arg Ala Pro Ser Val Gly Arg Arg Gly Ala Arg Ser Ser Arg Leu Gly
65 70 75 80

agc ggg cag agg cag agc gcc agt gag cgg gag aaa ctg cgc atg cgc 288
Ser Gly Gln Arg Gln Ser Ala Ser Glu Arg Glu Lys Leu Arg Met Arg
85 90 95

acg ctg gcc cgc gcc ctg cac gag ctg cgc cgc ttt cta ccg ccg tcc 336
Thr Leu Ala Arg Ala Leu His Glu Leu Arg Arg Phe Leu Pro Pro Ser
100 105 110

gtg gcg ccc gcg ggc cag agc ctg acc aag atc gag acg ctg cgc ctg 384
Val Ala Pro Ala Gly Gln Ser Leu Thr Lys Ile Glu Thr Leu Arg Leu
115 120 125

gct atc cgc tat atc ggc cac ctg tgc gcc gtg cta ggc ctc agc gag 432
Ala Ile Arg Tyr Ile Gly His Leu Ser Ala Val Leu Gly Leu Ser Glu
130 135 140

gag agt ctc cag cgc cgg tgc cgg cag cgc ggt gac gcg ggg tcc cct 480
Glu Ser Leu Gln Arg Arg Cys Arg Gln Arg Gly Asp Ala Gly Ser Pro
145 150 155 160

cgg ggc tgc ccg ctg tgc ccc gac gac tgc ccc gcg cag atg cag aca 528
Arg Gly Cys Pro Leu Cys Pro Asp Asp Cys Pro Ala Gln Met Gln Thr
165 170 175

cgg acg cag gct gag ggg cag ggg cag ggg cgc ggg ctg ggc ctg gta 576
Arg Thr Gln Ala Glu Gly Gln Gly Gln Gly Arg Gly Leu Gly Leu Val
180 185 190

tcc gcc gtc cgc gcc ggg gcg tcc tgg gga tcc ccg cct gcc tgc ccc 624
Ser Ala Val Arg Ala Gly Ala Ser Trp Gly Ser Pro Pro Ala Cys Pro
195 200 205

gga gcc cga gct gca ccc gag ccg cgc gac ccg cct gcg ctg ttc gcc 672
Gly Ala Arg Ala Ala Pro Glu Pro Arg Asp Pro Pro Ala Leu Phe Ala
210 215 220

gag gcg gcg tgc cct gaa ggg cag gcg atg gag cca agc cca ccg tcc 720
Glu Ala Ala Cys Pro Glu Gly Gln Ala Met Glu Pro Ser Pro Pro Ser
225 230 235 240

ccg ctc ctt ccg ggc gac gtg ctg gct ctg ttg gag acc tgg atg ccc 768
Pro Leu Leu Pro Gly Asp Val Leu Ala Leu Leu Glu Thr Trp Met Pro
245 250 255

ctc tcg cct ctg gag tgg ctg cct gag gag ccc aag 804
Leu Ser Pro Leu Glu Trp Leu Pro Glu Glu Pro Lys
260 265

<210> 63

<211> 215

<212> PRT

<213> Homo sapiens

<400> 63

Met Gly Ser Pro Arg Ser Ala Leu Ser Cys Leu Leu Leu His Leu Leu
1 5 10 15

Val Leu Cys Leu Gln Ala Gln Val Thr Val Gln Ser Ser Pro Asn Phe
20 25 30

Thr Gln His Val Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg
35 40 45

Arg Leu Ile Arg Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His
50 55 60

Val Gln Val Leu Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly
65 70 75 80

Asp Pro Phe Ala Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg
85 90 95

Val Arg Val Arg Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys
100 105 110

Lys Gly Lys Leu Ile Ala Lys Ser Asn Gly Lys Gly Lys Asp Cys Val
115 120 125

Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala
130 135 140

Lys Tyr Glu Gly Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg
145 150 155 160

Lys Gly Ser Lys Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys
165 170 175

Arg Leu Pro Arg Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu
180 185 190

Phe Leu Asn Tyr Pro Pro Phe Thr Arg Ser Leu Arg Gly Ser Gln Arg
195 200 205

Thr Trp Ala Pro Glu Pro Arg
210 215

<210> 64

<211> 645

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(648)

<400> 64

atg ggc agc ccc cgc tcc gcg ctg agc tgc ctg ctg ttg cac ttg ctg 48

Met Gly Ser Pro Arg Ser Ala Leu Ser Cys Leu Leu Leu His Leu Leu
1 5 10 15

gtc ctc tgc ctc caa gcc cag gta act gtt cag tcc tca cct aat ttt 96

Val Leu Cys Leu Gln Ala Gln Val Thr Val Gln Ser Ser Pro Asn Phe
20 25 30

aca cag cat gtg agg gag cag agc ctg gtg acg gat cag ctc agc cgc 144

Thr Gln His Val Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg
35 40 45

cgc ctc atc cgg acc tac caa ctc tac agc cgc acc agc ggg aag cac 192
Arg Leu Ile Arg Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His
50 55 60

gtg cag gtc ctg gcc aac aag cgc atc aac gcc atg gca gag gac ggc 240
Val Gln Val Leu Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly
65 70 75 80

gac ccc ttc gca aag ctc atc gtg gag acg gac acc ttt gga agc aga 288
Asp Pro Phe Ala Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg
85 90 95

gtt cga gtc cga gga gcc gag acg ggc ctc tac atc tgc atg aac aag 336
Val Arg Val Arg Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys
100 105 110

aag ggg aag ctg atc gcc aag agc aac ggc aaa ggc aag gac tgc gtc 384
Lys Gly Lys Leu Ile Ala Lys Ser Asn Gly Lys Gly Lys Asp Cys Val
115 120 125

ttc acg gag att gtg ctg gag aac aac tac aca gcg ctg cag aat gcc 432
Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala
130 135 140

aag tac gag ggc tgg tac atg gcc ttc acc cgc aag ggc cgg ccc cgc 480
Lys Tyr Glu Gly Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg
145 150 155 160

aag ggc tcc aag acg cgg cag cac cag cgt gag gtc cac ttc atg aag 528
Lys Gly Ser Lys Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys
165 170 175

cgg ctg ccc cgg ggc cac cac acc acc gag cag agc ctg cgc ttc gag 576
Arg Leu Pro Arg Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu
180 185 190

ttc ctc aac tac cgg ccc ttc acg cgc agc ctg cgc ggc agc cag agg 624
Phe Leu Asn Tyr Pro Pro Phe Thr Arg Ser Leu Arg Gly Ser Gln Arg
195 200 205

act tgg gcc ccg gaa ccc cga 645
Thr Trp Ala Pro Glu Pro Arg
210 215

<210> 65

<211> 212

<212> PRT

<213> Homo sapiens

<400> 65

Met Asp Tyr Leu Leu Met Ile Phe Ser Leu Leu Phe Val Ala Cys Gln
1 5 10 15

Gly Ala Pro Glu Thr Ala Val Leu Gly Ala Glu Leu Ser Ala Val Gly
20 25 30

Glu Asn Gly Gly Glu Lys Pro Thr Pro Ser Pro Pro Trp Arg Leu Arg
35 40 45

Arg Ser Lys Arg Cys Ser Cys Ser Ser Leu Met Asp Lys Glu Cys Val
50 55 60

Tyr Phe Cys His Leu Asp Ile Ile Trp Val Asn Thr Pro Glu His Val
65 70 75 80

Val Pro Tyr Gly Leu Gly Ser Pro Arg Ser Lys Arg Ala Leu Glu Asn
85 90 95

Leu Leu Pro Thr Lys Ala Thr Asp Arg Glu Asn Arg Cys Gln Cys Ala
100 105 110

Ser Gln Lys Asp Lys Lys Cys Trp Asn Phe Cys Gln Ala Gly Lys Glu
115 120 125

Leu Arg Ala Glu Asp Ile Met Glu Lys Asp Trp Asn Asn His Lys Lys
130 135 140

Gly Lys Asp Cys Ser Lys Leu Gly Lys Lys Cys Ile Tyr Gln Gln Leu
145 150 155 160

Val Arg Gly Arg Lys Ile Arg Arg Ser Ser Glu Glu His Leu Arg Gln
165 170 175

Thr Arg Ser Glu Thr Met Arg Asn Ser Val Lys Ser Ser Phe His Asp
180 185 190

Pro Lys Leu Lys Gly Lys Pro Ser Arg Glu Arg Tyr Val Thr His Asn
195 200 205

Arg Ala His Trp
210

<210> 66

<211> 636

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(639)

<400> 66

atg gat tat ttg ctc atg att ttc tct ctg ctg ttt gtg gct tgc caa 48

Met Asp Tyr Leu Leu Met Ile Phe Ser Leu Leu Phe Val Ala Cys Gln

1 5 10 15

gga gct cca gaa aca gca gtc tta ggc gct gag ctc agc gcg gtg ggt 96

Gly Ala Pro Glu Thr Ala Val Leu Gly Ala Glu Leu Ser Ala Val Gly

20 25 30

gag aac ggc ggg gag aaa ccc act ccc agt cca ccc tgg cgg ctc cgc 144

Glu Asn Gly Gly Glu Lys Pro Thr Pro Ser Pro Pro Trp Arg Leu Arg

35 40 45

cgg tcc aag cgc tgc tcc tgc tgc tcc ctg atg gat aaa gag tgt gtc 192

Arg Ser Lys Arg Cys Ser Cys Ser Ser Leu Met Asp Lys Glu Cys Val

50 55 60

tac ttc tgc cac ctg gac atc att tgg gtc aac act ccc gag cac gtt 240

Tyr Phe Cys His Leu Asp Ile Ile Trp Val Asn Thr Pro Glu His Val

65 70 75 80

gtt ccg tat gga ctt gga agc cct agg tcc aag aga gcc ttg gag aat 288

Val Pro Tyr Gly Leu Gly Ser Pro Arg Ser Lys Arg Ala Leu Glu Asn

85 90 95

tta ctt ccc aca aag gca aca gac cgt gag aat aga tgc caa tgt gct 336

Leu Leu Pro Thr Lys Ala Thr Asp Arg Glu Asn Arg Cys Gln Cys Ala

100 105 110

agc caa aaa gac aag aag tgc tgg aat ttt tgc caa gca gga aaa gaa 384

Ser Gln Lys Asp Lys Lys Cys Trp Asn Phe Cys Gln Ala Gly Lys Glu

115 120 125

ctc agg gct gaa gac att atg gag aaa gac tgg aat aat cat aag aaa 432

Leu Arg Ala Glu Asp Ile Met Glu Lys Asp Trp Asn Asn His Lys Lys

130 135 140

gga aaa gac tgt tcc aag ctt ggg aaa aag tgt att tat cag cag tta 480

Gly Lys Asp Cys Ser Lys Leu Gly Lys Lys Cys Ile Tyr Gln Gln Leu

145 150 155 160

gtg aga gga aga aaa atc aga aga agt tca gag gaa cac cta aga caa 528

Val Arg Gly Arg Lys Ile Arg Arg Ser Ser Glu Glu His Leu Arg Gln
165 170 175

acc agg tcg gag acc atg aga aac agc gtc aaa tca tct ttt cat gat 576
Thr Arg Ser Glu Thr Met Arg Asn Ser Val Lys Ser Ser Phe His Asp
180 185 190

ccc aag ctg aaa ggc aag ccc tcc aga gag cgt tat gtg acc cac aac 624
Pro Lys Leu Lys Gly Lys Pro Ser Arg Glu Arg Tyr Val Thr His Asn
195 200 205

cga gca cat tgg 636
Arg Ala His Trp
210

<210> 67

<211> 143

<212> PRT

<213> Homo sapiens

<400> 67

Met Gln His Arg Gly Phe Leu Leu Leu Thr Leu Leu Ala Leu Leu Ala
1 5 10 15

Leu Thr Ser Ala Val Ala Lys Lys Lys Asp Lys Val Lys Lys Gly Gly
20 25 30

Pro Gly Ser Glu Cys Ala Glu Trp Ala Trp Gly Pro Cys Thr Pro Ser
35 40 45

Ser Lys Asp Cys Gly Val Gly Phe Arg Glu Gly Thr Cys Gly Ala Gln
50 55 60

Thr Gln Arg Ile Arg Cys Arg Val Pro Cys Asn Trp Lys Lys Glu Phe
65 70 75 80

Gly Ala Asp Cys Lys Tyr Lys Phe Glu Asn Trp Gly Ala Cys Asp Gly
85 90 95

Gly Thr Gly Thr Lys Val Arg Gln Gly Thr Leu Lys Lys Ala Arg Tyr
100 105 110

Asn Ala Gln Cys Gln Glu Thr Ile Arg Val Thr Lys Pro Cys Thr Pro
115 120 125

Lys Thr Lys Ala Lys Ala Lys Ala Lys Lys Gly Lys Gly Lys Asp
130 135 140

<210> 68

<211> 429

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(432)

<400> 68

atg cag cac cga ggc ttc ctc ctc ctc acc ctc ctc gcc ctg ctg gcg 48
Met Gln His Arg Gly Phe Leu Leu Leu Thr Leu Leu Ala Leu Leu Ala
1 5 10 15

ctc acc tcc gcg gtc gcc aaa aag aaa gat aag gtg aag aag ggc ggc 96
Leu Thr Ser Ala Val Ala Lys Lys Lys Asp Lys Val Lys Lys Gly Gly
20 25 30

ccg ggg agc gag tgc gct gag tgg gcc tgg ggg ccc tgc acc ccc agc 144
Pro Gly Ser Glu Cys Ala Glu Trp Ala Trp Gly Pro Cys Thr Pro Ser
35 40 45

agc aag gat tgc ggc gtg ggt ttc cgc gag ggc acc tgc ggg gcc cag 192
Ser Lys Asp Cys Gly Val Gly Phe Arg Glu Gly Thr Cys Gly Ala Gln
50 55 60

acc cag cgc atc cgg tgc agg gtg ccc tgc aac tgg aag aag gag ttt 240
Thr Gln Arg Ile Arg Cys Arg Val Pro Cys Asn Trp Lys Lys Glu Phe
65 70 75 80

gga gcc gac tgc aag tac aag ttt gag aac tgg ggt gcg tgt gat ggg 288
Gly Ala Asp Cys Lys Tyr Lys Phe Glu Asn Trp Gly Ala Cys Asp Gly
85 90 95

ggc aca ggc acc aaa gtc cgc caa ggc acc ctg aag aag gcg cgc tac 336
Gly Thr Gly Thr Lys Val Arg Gln Gly Thr Leu Lys Lys Ala Arg Tyr
100 105 110

aat gct cag tgc cag gag acc atc cgc gtc acc aag ccc tgc acc ccc 384
Asn Ala Gln Cys Gln Glu Thr Ile Arg Val Thr Lys Pro Cys Thr Pro
115 120 125

aag acc aaa gca aag gcc aaa gcc aag aaa ggg aag gga aag gac 429
Lys Thr Lys Ala Lys Ala Lys Ala Lys Lys Gly Lys Gly Lys Asp
130 135 140

<210> 69

<211> 408

<212> PRT

<213> Homo sapiens

<400> 69

Met Ile Pro Gly Asn Arg Met Leu Met Val Val Leu Leu Cys Gln Val
1 5 10 15

Leu Leu Gly Gly Ala Ser His Ala Ser Leu Ile Pro Glu Thr Gly Lys
20 25 30

Lys Lys Val Ala Glu Ile Gln Gly His Ala Gly Gly Arg Arg Ser Gly
35 40 45

Gln Ser His Glu Leu Leu Arg Asp Phe Glu Ala Thr Leu Leu Gln Met
50 55 60

Phe Gly Leu Arg Arg Arg Pro Gln Pro Ser Lys Ser Ala Val Ile Pro
65 70 75 80

Asp Tyr Met Arg Asp Leu Tyr Arg Leu Gln Ser Gly Glu Glu Glu Glu
85 90 95

Glu Gln Ile His Ser Thr Gly Leu Glu Tyr Pro Glu Arg Pro Ala Ser
100 105 110

Arg Ala Asn Thr Val Arg Ser Phe His His Glu Glu His Leu Glu Asn
115 120 125

Ile Pro Gly Thr Ser Glu Asn Ser Ala Phe Arg Phe Leu Phe Asn Leu
130 135 140

Ser Ser Ile Pro Glu Asn Glu Ala Ile Ser Ser Ala Glu Leu Arg Leu
145 150 155 160

Phe Arg Glu Gln Val Asp Gln Gly Pro Asp Trp Glu Arg Gly Phe His
165 170 175

Arg Ile Asn Ile Tyr Glu Val Met Lys Pro Pro Ala Glu Val Val Pro
180 185 190

Gly His Leu Ile Thr Arg Leu Leu Asp Thr Arg Leu Val His His Asn
195 200 205

Val Thr Arg Trp Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp
210 215 220

Thr Arg Glu Lys Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His
225 230 235 240

Leu His Gln Thr Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg
245 250 255

Ser Leu Pro Gln Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu
260 265 270

Val Thr Phe Gly His Asp Gly Arg Gly His Ala Leu Thr Arg Arg Arg
275 280 285

Arg Ala Lys Arg Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys
290 295 300

Asn Lys Asn Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val
305 310 315 320

Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr
325 330 335

Cys His Gly Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr
340 345 350

Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile
355 360 365

Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu
370 375 380

Tyr Leu Asp Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met
385 390 395 400

Val Val Glu Gly Cys Gly Cys Arg
405

<210> 70

<211> 1224

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1227)

<400> 70

atg att cct ggt aac cga atg ctg atg gtc gtt tta tta tgc caa gtc 48

Met Ile Pro Gly Asn Arg Met Leu Met Val Val Leu Leu Cys Gln Val
1 5 10 15

ctg cta gga ggc gcg agc cat gct agt ttg ata cct gag acg ggg aag 96

Leu Leu Gly Gly Ala Ser His Ala Ser Leu Ile Pro Glu Thr Gly Lys

20

25

30

aaa aaa gtc gcc gag att cag ggc cac gcg gga gga cgc cgc tca ggg 144

Lys Lys Val Ala Glu Ile Gln Gly His Ala Gly Gly Arg Arg Ser Gly

35

40

45

cag agc cat gag ctc ctg cgg gac ttc gag gcg aca ctt ctg cag atg 192

Gln Ser His Glu Leu Leu Arg Asp Phe Glu Ala Thr Leu Leu Gln Met

50

55

60

ttt ggg ctg cgc cgc cgc ccg cag cct agc aag agt gcc gtc att ccg 240

Phe Gly Leu Arg Arg Arg Pro Gln Pro Ser Lys Ser Ala Val Ile Pro

65

70

75

80

gac tac atg cgg gat ctt tac cgg ctt cag tct ggg gag gag gag gaa 288

Asp Tyr Met Arg Asp Leu Tyr Arg Leu Gln Ser Gly Glu Glu Glu Glu

85

90

95

gag cag atc cac agc act ggt ctt gag tat cct gag cgc ccg gcc agc 336

Glu Gln Ile His Ser Thr Gly Leu Glu Tyr Pro Glu Arg Pro Ala Ser

100

105

110

cgg gcc aac acc gtg agg agc ttc cac cac gaa gaa cat ctg gag aac 384

Arg Ala Asn Thr Val Arg Ser Phe His His Glu Glu His Leu Glu Asn

115

120

125

atc cca ggg acc agt gaa aac tct get ttt cgt ttc ctc ttt aac ctc 432

Ile Pro Gly Thr Ser Glu Asn Ser Ala Phe Arg Phe Leu Phe Asn Leu

130

135

140

agc agc atc cct gag aac gag gcg atc tcc tct gca gag ctt cgg ctc 480

Ser Ser Ile Pro Glu Asn Glu Ala Ile Ser Ser Ala Glu Leu Arg Leu

145

150

155

160

ttc cgg gag cag gtg gac cag ggc cct gat tgg gaa agg ggc ttc cac 528

Phe Arg Glu Gln Val Asp Gln Gly Pro Asp Trp Glu Arg Gly Phe His

165

170

175

cgt ata aac att tat gag gtt atg aag ccc cca gca gaa gtg gtg cct 576

Arg Ile Asn Ile Tyr Glu Val Met Lys Pro Pro Ala Glu Val Val Pro

180

185

190

ggg cac ctc atc aca cga cta ctg gac acg aga ctg gtc cac cac aat 624

Gly His Leu Ile Thr Arg Leu Leu Asp Thr Arg Leu Val His His Asn

195

200

205

gtg aca cgg tgg gaa act ttt gat gtg agc cct gcg gtc ctt cgc tgg 672
Val Thr Arg Trp Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp
210 215 220

acc cgg gag aag cag cca aac tat ggg cta gcc att gag gtg act cac 720
Thr Arg Glu Lys Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His
225 230 235 240

ctc cat cag act cgg acc cac cag ggc cag cat gtc agg att agc cga 768
Leu His Gln Thr Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg
245 250 255

tgc tta cct caa ggg agt ggg aat tgg gcc cag ctc cgg ccc ctc ctg 816
Ser Leu Pro Gln Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu
260 265 270

gtc acc ttt ggc cat gat ggc cgg ggc cat gcc ttg acc cga cgc cgg 864
Val Thr Phe Gly His Asp Gly Arg Gly His Ala Leu Thr Arg Arg Arg
275 280 285

agg gcc aag cgt agc cct aag cat cac tca cag cgg gcc agg aag aag 912
Arg Ala Lys Arg Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys
290 295 300

aat aag aac tgc cgg cgc cac tgc ctc tat gtg gac ttc agc gat gtg 960
Asn Lys Asn Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val
305 310 315 320

ggc tgg aat gac tgg att gtg gcc cca cca ggc tac cag gcc ttc tac 1008
Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr
325 330 335

tgc cat ggg gac tgc ccc ttt cca ctg gct gac cac ctc aac tca acc 1056
Cys His Gly Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr
340 345 350

aac cat gcc att gtg cag acc ctg gtc aat tet gtc aat tcc agt atc 1104
Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile
355 360 365

ccc aaa gcc tgt tgt gtg ccc act gaa ctg agt gcc atc tcc atg ctg 1152
Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu
370 375 380

tac ctg gat gag tat gat aag gtg gta ctg aaa aat tat cag gag atg 1200
Tyr Leu Asp Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met

385	390	395	400	
gta gta gag gga tgt ggg tgc cgc				1224
Val Val Glu Gly Cys Gly Cys Arg				
405				
<210> 71				
<211> 24				
<212> DNA				
<213> Artificial Sequence				
<220>				
<221>				
<222>				
<223>				
<400> 71				
gccccgcgtc caactgctct gatg				24
<210> 72				
<211> 24				
<212> DNA				
<213> Artificial Sequence				
<220>				
<221>				
<222>				
<223>				
<400> 72				
tgcctacggt ggtgcgccct ctgc				24
<210> 73				
<211> 22				
<212> DNA				
<213> Artificial Sequence				
<220>				
<221>				
<222>				
<223>				
<400> 73				
gaagcgcaac agggccatca cg				22
<210> 74				
<211> 22				
<212> DNA				
<213> Artificial Sequence				
<220>				
<221>				
<222>				
<223>				

<400> 74
ccacgtcacg caggtcccgt tc 22

<210> 75
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<221>
<222>
<223>

<400> 75
gatcctgttc tctgcctctg ga 22

<210> 76
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<221>
<222>
<223>

<400> 76
tcattccactt tgtccaccg ag 22

<210> 77
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<221>
<222>
<223>

<400> 77
ttctcgtct tggcctttg g 21

<210> 78
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<221>
<222>
<223>

<400> 78
gctggatctt cgtaggtcc g 21

<210> 79
<211> 19
<212> DNA
<213> Artificial Sequence
<220>
<221>
<222>
<223>
<400> 79
ggcaagctga ccctgaagt

19

<210> 80
<211> 19
<212> DNA
<213> Artificial Sequence
<220>
<221>
<222>
<223>
<400> 80
gggtgctcag gtagtggtt

19